

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification 5 : C12N 15/11, C12P 21/08 C12Q 1/68, C12N 15/62 C07K 15/28</p>		A2	<p>(11) International Publication Number: WO 94/01548 (43) International Publication Date: 20 January 1994 (20.01.94)</p>
<p>(21) International Application Number: PCT/GB93/01467 (22) International Filing Date: 13 July 1993 (13.07.93)</p>		<p>(74) Agent: BIZLEY, Richard, Edward; Hepworth Lawrence Bryer & Bizley, 2nd Floor Gate House South, West Gate, Har- low, Essex CM20 1JN (GB).</p>	
<p>(30) Priority data: 9214857.6 13 July 1992 (13.07.92) GB</p>		<p>(81) Designated States: AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p>	
<p>(71) Applicant (for all designated States except US): MEDICAL RESEARCH COUNCIL [GB/GB]; 20 Park Crescent, London W1N 4AL (GB).</p>		<p>Published <i>Without international search report and to be republished upon receipt of that report.</i></p>	
<p>(72) Inventors; and (75) Inventors/Applicants (for US only) : SIBSON, David, Ross [GB/GB]; 37 Grimsdells Lane, Amersham, Bucking- hamshire HP6 6HF (GB). GROSS, Jacqueline [GB/GB]; 47 Boxmoor Road, Kenton, Middlesex HA3 8LH (GB). HADFIELD, Kathryn, Mary [GB/GB]; 5 Carlisle Ter- race, St Ives, Huntingdon, Cambridgeshire PE17 4PQ (GB). HOWELLS, David [GB/GB]; 77 Puttocks Drive, Welham Green, Hatfield, Hertfordshire AL9 7LW (GB). STARKEY, Michael [GB/GB]; 27 Creasy Close, Abbots Langley, Hertfordshire WD5 0HS (GB). KELLY, Maria [IE/GB]; 24A Oxford Road, Ealing, London W5 3ST (GB). SHAW, Diana [GB/CA]; 342 Glacier Hall, Uni- versity of Calgary, 2500 University Drive NW, Calgary, Alberta T2N 1N4 (CA).</p>			
<p>(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE NARROW</p>			
<p>(57) Abstract</p> <p>This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.</p>			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AT	Austria	FR	France	MR	Mauritania
AU	Australia	GA	Gabon	MW	Malawi
BB	Barbados	GB	United Kingdom	NE	Niger
BE	Belgium	GN	Guinea	NL	Netherlands
BF	Burkina Faso	GR	Greece	NO	Norway
BG	Bulgaria	HU	Hungary	NZ	New Zealand
BJ	Benin	IE	Ireland	PL	Poland
BR	Brazil	IT	Italy	PT	Portugal
BY	Belarus	JP	Japan	RO	Romania
CA	Canada	KP	Democratic People's Republic of Korea	RU	Russian Federation
CF	Central African Republic	KR	Republic of Korea	SD	Sudan
CG	Congo	KZ	Kazakhstan	SE	Sweden
CH	Switzerland	LI	Liechtenstein	SI	Slovenia
CI	Côte d'Ivoire	LK	Sri Lanka	SK	Slovak Republic
CM	Cameroon	LU	Luxembourg	SN	Senegal
CN	China	LV	Latvia	TD	Chad
CS	Czechoslovakia	MC	Monaco	TG	Togo
CZ	Czech Republic	MG	Madagascar	UA	Ukraine
DE	Germany	ML	Mali	US	United States of America
DK	Denmark	MN	Mongolia	UZ	Uzbekistan
ES	Spain			VN	Viet Nam
FI	Finland				

1
HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN
ADRENAL TISSUE, PLACENTA OR BONE MARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may 10 contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

15 There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed 20 mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated 25 sequences or non-coding sequences in an approach which depends upon sequences or non-coding sequences in an approach which depends upon genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science 35 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambiguously classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs identified in this way were further characterised and found to be useful in a variety of standard applications, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.

A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 5 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each 10 reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 15 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogenous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered 20 to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

25

(a) preparing a mixture comprising a heterogenous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;

30

(b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;

35

(c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and

(d) carrying out an extension synthesis in the mixture produced in step (c).

40

Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

5

Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually, therefore, all DNA species will be present at the same concentration.

15

The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for each DNA population.

20

In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirety, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

25

30 In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogenous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid population is treated by:

35

40 (a) subjecting the nucleic acid to the action of a reagent,

preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

5

(b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adaptored cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

10

(c) selecting and separating only those adaptored cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

15

A preferred endonuclease for use in step (a) of the above process is Fok 1.

20

An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

25

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin

reaction in selecting and separating desired adaptored molecules.

30

Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adaptored molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

35

Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

40

and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adaptored end of 5 the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand 10 making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during 15 subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide 20 also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot 25 interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it 30 is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from 35 the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adaptorizing" process can be used to generate categories or 40 subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

10

- (a) a sequence selected from SEQ ID Nos 1 to 1193;
- (b) an allelic variation of a sequence as defined in (a); or
- 15 (c) a sequence complementary to (a) or (b).

20

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% homology to a human sequence known per se.

25

In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, for example, to the following: Melting temperature of hybrids - Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci., 48 p1390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, p1 (1985).

40

The present invention also envisages DNA constructs comprising fragments or sequences as referred to above with a control or regulatory sequence.

The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that 5 when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or sequence in accordance with the invention may be released by the 10 endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

15 Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

20 Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.

25 Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved 30 using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal antibodies using standard techniques.

35 Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and Herzenberg, L. A., Handbook of Experimental Immunology : Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

D. M. et al., p108 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic *Bacillus subtilis*, eukaryotic yeast, mammalian cows milk vectors, and other methods known in the art.

10 The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

15 It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate 20 sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate 25 indication of where the beginnings and ends of the component sequences are.

In contrast to investigations hitherto, where gene fragments (sequence 30 fragments) could only be identified through some known characteristic [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having ability to encode expressed proteins which could later be detected by 35 functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present invention are entirely underivable and unpredictable from the prior 40 art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

used as a means for determining the existence of new members of existing gene families, new human genes when previously only non-human genes were known and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparent. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alessio, J. M., et al., Focus (Gibco B.R.L.) 9 p1 (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltz, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targeting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Prokaryotic, and lower or higher eukaryotic hosts may be selected as the host for expression and higher

eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. Gene 40 p183 1985),
5 Shimuzu, Y et al., Gene 65, p141 (1988), Straus, D. and Gilbert, W. Proc. Natl. Acad. Sci. 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

10 The proteins thus-expressed can be screened for activities of therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith,
15 D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)).

20 Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. Nature 353 pp605-607 (1991), Rudensky, A., Y., et al., Nature 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable,
25 although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)). The immobilised polypeptide can then be used to affinity purify the antibodies.
30 Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide.
35 Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase
40 (Nagai, K., and Thogersen, H., C. Methods Enzmol. 153 p461-481 (1987). Another alternative is raise monoclonal antibodies against the purified protein.

The antibodies can be used for localising *in situ*, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg 5 cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in combination to isolate particular populations of cells. These in turn 10 can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease 15 states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given 20 individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, 25 the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference, 30 Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

35 Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA 40 will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

clone.

This invention will now be further described and illustrated by means of the following Examples.

5

All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 10 (1985)).

Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to 15 15 week menstrual age foetuses and then snap frozen in liquid nitrogen before storing in bijou bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, 20 using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the 25 manufacturer's instructions, except that centrifugation was performed for 36 hours and the RNA obtained was finally desalting and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA⁺ (mRNA) was isolated from 200 to 400 µg of the total RNA by binding it to 30 magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA 35 were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and 40 then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's

instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

5 The column eluate was adjusted to 10 mM Mg²⁺ and then the purified cDNA was restricted by the action of 1 unit per 10 µl of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

10 The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

15 The adaptors used were oligonucleotides 5' N,N,N,N,TCCTTCTCCTGCGACAGACA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTCGCAGGAGAACAGGA (SEQ ID: 1195) and 5' AAN,N,TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5' TTN,N,TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1197) each with the complementary 20 5' biotinylated strand GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198). These pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added MgCl₂ to 10mM, ATP to 10mM and 0.025 units/µl 25 of T4 DNA ligase. The oligonucleotide 5' biotinylated GTTCTCGGAGCACTGTCCGAGA, (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume 25 was 90 µl which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

30 Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

35 The column eluate was adjusted to 25mM Mg²⁺, 0.5mM dNTPs in a final volume of 200 µl. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200 µl of 40 streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary to the 5'

.GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

5 Un-biotinylated cDNAs were washed from the beads with 400 μ l each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg²⁺. The beads were then resuspended in 240 μ l of the final buffer including additionally 0.5 mM dNTPs and divided into 4x60
10 μ l.

Four of the 60 μ l aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adaptored fragments. 2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAA
15 (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq DNA polymerase were added to each reaction and 16 cycles of alternate denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes
20 and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 μ l of resuspended beads were added to each reaction to remove the biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an
25 S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one
35 of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCAGACTGTCCGAGAC SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to
40 behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8 μ l or 12.5 % whichever was the larger 5 but not exceeding 12 μ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM Mg²⁺, 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40 μ l. Apart from when an initial amplification with 2 pmoles of each primer was performed, 20 pmoles of each primer were used. Cycles of 10 amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. 15 Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

20 The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60 μ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris 25 HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. 30 (Nucl. Acids Res. 18, p6156 (1990)). Different cohesive ends were produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. To 75 μ l or 75 % of the column eluate, whichever was least, were added 9.5 μ l of 100mM TrisHCl pH7.4, 100 mM MgCl₂, and 9.5 μ l of 0.5 mM dTTP. 35 16 units of T4 DNA polymerase were added and the reaction incubated in a water bath at 37°C for 30 minutes. The enzyme was removed by extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as 40 described above.

The E.coli plasmid cloning vector pBluescript KS+ (Åltting-Meese, M. A.

and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptoring the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG
5 (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACACTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptoring were performed according to standard 10 procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and 15 transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG 20 L-agar plates containing 50µg/ml ampicillin and 10µg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100µl of L-broth and 50µg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100µl of 50% or 30% glycerol was added to plates which were archived at -20°C or -80°C, 25 respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). 30 Bacteria for this purpose were either grown on L-agar plates containing 50µg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive. In all cases, cDNA inserts were amplified for sequencing by PCR 35 (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the 40 plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40 μ l reactions containing 2.5mM Mg²⁺, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of AmpliTaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 5 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of 10 successful reactions were then recovered for single-stranded sequencing by binding them to streptavidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic work-station attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. 20 Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluorescein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for 25 the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" (TED). In both cases, files of called bases were entered into a Sybase™ database. Entering data entailed automatically removing vector 30 and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the publicly available databases, GENBANK and SWISSPROT. Searches were 35 performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the 40 above procedure.

Example 2

A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTGACAAGCTTGAATTTCGGCCGC(T)_n, (SEQ ID: 1210) was used at 1 μ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5 μ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100 μ l with water.

PCRs were then performed in reactions containing 1 μ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin, 200 μ M dNTPs, 10 uCi a³²P dCTP, 1 μ M each of the primers 11AD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°C for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

WO 94/01548

20

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

Example 3

5 cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into E.coli Y1090 and plated out for colour selection of recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., 10 Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyocarcoma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

15 Clear plaques from each library were resuspended in 5 µl of Tris-HCl pH 8, 1 mM EDTA. 2 µl of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that 20 the oligonucleotides used as primers for the lambda gt11 clones were 5' GGTGGCCACGACTCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

25 Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

30 Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

35 The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

(1) GENERAL INFORMATION

(i) APPLICANT

- (A) NAME: MEDICAL RESEARCH COUNCIL
5 (B) STREET: 20 PARK CRESCENT
(C) CITY: LONDON
(E) COUNTRY: ENGLAND
(F) POSTAL CODE: W1N 4AL

10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

(iv) COMPUTER READABLE FORM:

15

- (A) MEDIUM TYPE: DISKETTE
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: EXTRACT

20

(2) INFORMATION FOR SEQ ID :1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1:

GCCGATTCTGT GACCAAGAAAG GCTCTGTGCA TTGGGGTTTT CCAGGAGACT	50
35 CAAAAGCTGA AGAACGGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA	100
ATAAAACAAGC AAAGCGGAGG AACCCAGACA GCCCTTGTCC AAAGCCATAC	150
40 CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT	200
GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCAAT ATATCATATA	250

22

TATATATATA CACA

264

(2) INFORMATION FOR SEQ ID :2:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :2:

15.	AGGAACATGT GTTTATTCCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT	50
	GCCAGGGCAG CATTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC	100
	CTGGGGAGGG GGTCAATTGTT CTCT	124

20

(2) INFORMATION FOR SEQ ID :3:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :3:

	ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAAGC	50
35	TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC	100
	TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAAACGA ACTGAGATGC	150
	AAATTAAGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA	200
40	GCACAATCAC TAGTGTAGAG ATAACAGAAAT TTCTGAATTC CCTGAAAGCA	250

23

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATAACG	300
TCACATATTA CGAACTGATA ACATAAGGTA AAC	333

5 (2) INFORMATION FOR SEQ ID :4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC	50
GGAGCTCAAG GATCAGAGTA ACACAATTTC CACTTTTCT GTCTTTATGT	100
20 AAGAAGAAC TGCCTAGATG ACGGGGCCTC CTTCTTCAAA CAGGAATTTC	150
TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCCCT TGCCCCCAT	200

25 (2) INFORMATION FOR SEQ ID :5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - 30 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA	50
AGATTTGCCA AATTGTAGCC TACTGGATTG CGGTTCTCTT GACATCTCTT	100
40 TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA	150

24

ATTAACCAAGGGAGGATT AAGAATAATG AAAAGAGAAA AATCAAGAAA 200
GCACAATCAC TAG 213

5 (2) INFORMATION FOR SEQ ID :6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG 50
GAAGTTTAA GCTAAGATTT GCCAAATTGT AGCCTACTGG ATTCCGGTTC 100
20 TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACCTCCC GAGTATAAAC 150
GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG 200
25 AAAATCAAG AAAGCACAAT CACTAGTGTGAGATAACAG AATTCTGAA 250
TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT 300
GTGGCCCATA CGTCACATAT TAGGAACGTGA TAACATAAGG TAAAC 345

30 (2) INFORMATION FOR SEQ ID :7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

25

	TCCATTTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCTTG	50
	GGGTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCA	100
5	GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT	150
	TTCTTTCC	159

(2) INFORMATION FOR SEQ ID :8:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :8:

20

	ATATTTCAAT CGAACAAAAA GGAAACTTTT TTTGAACCTTA TTGAGGCTCT	50
	ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTCCT	100
25	TGCCTGGCTG GGGGTTTGAT TCGC	124

(2) INFORMATION FOR SEQ ID :9:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :9:

40

	CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA	50
	TCCGGATCAC CTGTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG	100

WO 94/01548

26

ACCGGGATGC AGTGTCAAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG 150
 GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCCCTGTC 200
 5 CCAGAGCCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA 250
 GAAAATAGA 259

(2) INFORMATION FOR SEQ ID :10:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :10:

20

GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCCAGGG CCCTCAAGAA 50
 GCTCCTGCAC ACAATAAACG CGCCCTCGTT CTTTAGCAAG TCTGCTCCCT 100
 25 CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA 150
 GACTACTTTA TTGGATGCCG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA 200
 CTGTGACAAG GGGCCC 216

30

(2) INFORMATION FOR SEQ ID :11:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :11:

27

CACACTTCTT AAGATAACATC AAGTACTAGT GATCTTGCT AGCAGTTATG 50
CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCGTGA 100
5 AAGTTGAAAG AAAAAGTTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT 150
GCAGGGCTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG 200
GGATG 205

10

(2) INFORMATION FOR SEQ ID :12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :12:

TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC 50
AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT 100
25 CACCGTCCCTT CCGAGCTCCA CGGGCACTCC ACTCTCGAAC TTCAGTCGAA 150
GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG 200
30 TAAGTCCATG CTGCGTCAAA TATTCCACTA TATTCCACAC TACTGCTGGA 250
TATGCCATTC TCGGTGA 267

35

(2) INFORMATION FOR SEQ ID :13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :13:

5 GCCTCATCAG GTTGCCCAAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG 50
GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTG ACGGCCTCAG 100
CAATGTGAAG CTGAAC 116

10 (2) INFORMATION FOR SEQ ID :14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

TTCGAACTTA CCAGCATCAT GTTGGTCTC TTCTGTATGGT CAAACTTCAA 50
CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCCAGG 100
25 CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAATC ACATGACACT 150
ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATAACATCTA 200
30 AGGGGTGCAA GGACCAGGCT TTGATTTCAA ATTATAATCT AATGCTCACT 250
CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA 296

(2) INFORMATION FOR SEQ ID :15:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

29

(xi) SEQUENCE DESCRIPTION: SEQ ID :15:

	CGTCAGTGTG CTACTTCACA TCATTAGCGA GGCCCAGAAA CTTGAACAGG	50
5	AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC	100
	CAAACTCGAT TCAAAGAGCA ATA	123

(2) INFORMATION FOR SEQ ID :16:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :16:

20

	CAACACATTA GTGCATCAAT ATGAATTACT TGTTAAAAAA ATCAAATGCT	50
	GGCATTGTCA GAAAATTAA ACAGGTTTAT TTATAATTAT CATAAAGTTG	100
25	ACGCTGAAAC TTGTTCACTG AAACATTTA ACTTGCATTA ATGCTTTACG	150
	TCTCCGCATT TATATTTAA ATTCAACACAC AAATGAAATG GAAAAGTGC	200
	CAATACCTGA TTTCTGTCCC TATTTTCAC TCGCAATCAT ATACTTAGTA	250
30	CTTTTGACTC TA	262

(2) INFORMATION FOR SEQ ID :17:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :17:

	TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG	50
5	AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT	100
	TGAAAGTAAG TTTTGAAACA GGACTCGTGG AGATTCTAAA CCTTGCATTT	150
10	TCAAGAAACG TGCATCAGC	169

(2) INFORMATION FOR SEQ ID :18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :18:

	AGGGGCACCA TTACCATCCA TCTGACATCG CATTCCATA GAAATGGCCA	50
25	AAGAAAGAAG GTCCTGGTAG GTTTTCATA GAAAGACTCA AAAAGTTCAA	100
	CCTTTGATGC TATGCCAG CCCAATACAA AACTACACAG AACAAAGCAA	150
	TTATTAAT ACTGGCTTCG GTTTCTTTT TTCCCTTGCA AAGTTTCCTA	200
30	CATATATGTC TTTTACAGTA T	221

(2) INFORMATION FOR SEQ ID :19:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

31

(xi) SEQUENCE DESCRIPTION: SEQ ID :19:

	TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTCACAA	50
5	TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTT ATGTGTTGCT	100
	TCTATTTAC CTGAAATTGT AGATATAGGG TAATC	135

(2) INFORMATION FOR SEQ ID :20:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :20:

20	GTTATCTATC TATCTTGCAG TTTACCTATC TGATCTGATC TCTGTAATTA	50
	TAGTTCTGTC ATTTAAAATA TACTATTTAA ATCTAATTTC TACATTCAA	100
25	AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG	150
	TTATTTTCA GAATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT	200
	TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTAA AAAAAATTGT	250
30	ATAATTTGT GATAATGTAG TTTCCAAAA CACATTTAGA AAGCATTATG	300
	TTATTAGTAA ATGA	314

35 (2) INFORMATION FOR SEQ ID :21:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :21:

5 TCTTCGCATC ACGCACTACA GATACTCTTT CTGTACTTGC TTAATCTGCT 50
 TTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC 100
 TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT 150
10 TCCTCTTTCA ATATTTCTGT TTCTTGCC 178

(2) INFORMATION FOR SEQ ID :22:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 188 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :22:

25 ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT 50
 ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA 100
 GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTT 150
30 TTTCTTAAAA CAACACACTT ATTATCTTAC AAATCTGT 188

(2) INFORMATION FOR SEQ ID :23:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

33

(xi) SEQUENCE DESCRIPTION: SEQ ID :23:

	TTCCANCTAA ACATCCAATA TNTCNNTTAN TGCTTTATA TTTTTNAAAT	50
5	GTTAAAACCC CTATACCACC TTTTGGGAAT GTTTAAATT CTCCAATTTC	100
	TCGTTATATA GGATCAACCA ACTAAGAAAA GATTTTATCA ATTGAATTGA	150
	GG	152
10		

(2) INFORMATION FOR SEQ ID :24:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| | (A) LENGTH: 83 base pairs |
| 15 | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :24:
----	--

	ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTCA ACCAACTTCA	50
25	ACTTTGCAC ACTTTTTCAA CGGTCCCACC ACA	83

(2) INFORMATION FOR SEQ ID :25:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 30 | (A) LENGTH: 176 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35	(xi) SEQUENCE DESCRIPTION: SEQ ID :25:
----	--

	AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCTTGCCT GTCAAATNCA	50
40	ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT	100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAAC CATNTGCACC 150
 CTACATCTGG CTGACATTAA CATTAA 176

5 (2) INFORMATION FOR SEQ ID :26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAAATA GGTACGCTTT TAAAATATTAA GAACAGAAAA 50
 GCTACAAATA AATNGAGCAA TGCTTTAAA ATCATCTTG TTTTATAGAC 100
 20 TTTTCCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT 150
 TTAAGTACTG ACGAAGAAGA CTAAAACAAT CATTAACTAA CAATATTTAA 200
 25 AAGGATCATA TAGTCGACTT TTAAAACANC CC 232

(2) INFORMATION FOR SEQ ID :27:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACCTCTCT AAGGAGAATG 50
 40 GCCCAATCTT CCCAAGTCCA CACAGGAGGG AAACATTGTT TGCCTAAATA 100

35

CGCAATGCAA AATTTNNNTAT CTTGGCTTAA TACNNCGACG TTTTATTTCG 150

AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC 192

5 (2) INFORMATION FOR SEQ ID :28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT 50

TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTAACCC CTCATAAAAT 100

20 GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT 150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT 200

25 T 201

(2) INFORMATION FOR SEQ ID :29:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :29:

40 AACCTAAGGC AGTTGACCCCC ACCTTCCAAC ATGTTTCAC TTTATTGGCC 50

CCTCCCTACA TTGGGGTTAG GTTCCATTG ATTTGCACAA TAATGACTTT 100

WO 94/01548

36

ATTTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTA TCATAGAACT 150
 AACTATTTA ATTACATATA ATGTAACCAA TGGAGAGATT TATAGAGAAT 200
 5 TTTGTCCCCC TGTCATATAC TCCATTTCGA AGACAGATAT GATAGAACTA 250
 GAAATTAAGT TGCATTTCTG CAACT 275

(2) INFORMATION FOR SEQ ID :30:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :30:

20 GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC 50
 ATTCAATCAAC AAGATTTCGA ATGGAATATT CCAGAAATTT CTGAGCCATC 100
 25 TGATCACAAAC AACCGTCTTT GA 122

(2) INFORMATION FOR SEQ ID :31:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :31:

GGATTTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT 50
 40 AGAGATCTTC CCAATGAACC TCAATACACG ATCGTAATAC TCGCACAATG 100

37

AAATGTTAAG TATGATTCTA GACTTCAGTG ACTATCACAA TGATATTTTC 150

TCGATCGCAC TAGTGCACAA CAAAACACGA TGAGTGCATT GTGAAAC 197

5 (2) INFORMATION FOR SEQ ID :32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG 50

TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC 97

20 (2) INFORMATION FOR SEQ ID :33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTAAAGCTACAAT AGTTATATAC CAAAGCAATA 50

35 CCTATTACAT GCTTTACACA ATCCCAGGAA AAAATAATTT AATAGCTCCT 100

AATCCCTGAT GCAAGGCAGT TCAAAGCACC CGCACAAAC TCCATGAAAC 150

40 AACATACAAT ACATCATTAA AATAACATAA ACGACTTTCA CACACTTGAC 200

CTAGGAAAAA ATAAAATCCA TACAACCACA GCTAAAAACA TGTAAAGATT 250

WO 94/01548

38

260

CACAAATAAGA

(2) INFORMATION FOR SEQ ID :34:

- 5 (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :34:

15	GGACNTGCGC NNNANNNA GCCANTGAAC NCAGGCCACCA NTGCAAGAAG	50
	ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT	100
20	GATCCAAAAT ACCTTCCTTN CCAAGCCCCGG GGTNNNNGAT AAGGTGTGGA NTTNGGTTAA AGACAAGG	150 168

(2) INFORMATION FOR SEQ ID :35:

- 25 (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :35:

35	CTCGNACACT GTGGAGAGCC TGC GNNNNNN NNGTNTACT CAGGGGGACG	50
	AAAAGGAGNN GAANAAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT	100
	GCTNNNGTGG TCCCTTAGNA CCCGAGNAGG TGGGCGCGAG GTGAANAAGG	150
40	TGC NNGTGCG AGAGTGC CGTG ATT	173

39

(2) INFORMATION FOR SEQ ID :36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :36:

AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA	50
CAACTAATAA TGATTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA	100
GTTTGCTAA CCTTGGTAAG CTTGTTTACC GTT	134

20

(2) INFORMATION FOR SEQ ID :37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :37:

TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA	50
ATTTGTGTTT ATACAACAA TAATGACCTT TTATTTGCTC AGTACAGACN	100
GATTACAAT GAAAGTTTG CTAACCTTGG TAAGCTTGT AACCCTTAC	150
ATGACTTCTT	160

40

(2) INFORMATION FOR SEQ ID :38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs

WO 94/01548

40

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :38:

	CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAAATCCCA CCCTCACACG	50
10	ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGGACT	100
	CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC	140

15 (2) INFORMATION FOR SEQ ID :39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :39:

	AGCAAGTATC ANNNNNNNNN ATACATTGA ATTCAAGTTG TTTTTGTCA	50
	AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG	100
30	GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTG GCCACCACCG	150
	CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAAN NATTANGGA	200
35	AAA	203

(2) INFORMATION FOR SEQ ID :40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

41

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

	GAAAAGCNNN NNNNNNNNGGC TTAAAGAACCA ATATGCTGAG ATGGAGAAGG	50
10	ACCTAGCGAA ANTNNNAACC TTTTAAGAAC TTGAANNACA ACAATCACAA	100
	ACTAATGAGA AGATGTTCAC CTCTCTCCTG AAAACTATGC CCACCAGACC	150
	GTTCAGCCTC TGCTCAAGCT	170

15 (2) INFORMATION FOR SEQ ID :41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

	GCTGCATGTT TCCTTGNATT TGAGCTTGAA AGTCAGAGC TGTTTACCCA	50
30	AAAAGGGAGC CAATAGAGAT CTTCCCAATG AACCTCAAAC ACGTCGTAAT	100
	ACTCGCACAA TGAAATGTCA AGTATGATT TAGACTTCAC TGACTCATCA	150
	CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA	200
35	ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTT AAATNCATAG	250
	AAATTTGATT TGTAATAAAA	270

(2) INFORMATION FOR SEQ ID :42:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs

42

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :42:

	AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC	50
10	CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT	100
	AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC	150
15	ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT	200
	GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTAA TCTTA	245

(2) INFORMATION FOR SEQ ID :43:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 124 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :43:

30	TACACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC	50
	TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA	100
35	ATGAAGACAC TTTACACTT TCGG	124

(2) INFORMATION FOR SEQ ID :44:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 144 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

43

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

	GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG	50
10	GCAAATTCCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTAA	100
	AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA	144

(2) INFORMATION FOR SEQ ID :45:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25	ACTGATTCCNN NNTGAAAATA CCCCCTTTCT CCATTAGTGG CATGCTCATT	50
	CAGCTCTTAT CTTTATATTTC CAGTAAGTTA TTTTGCTCTC ACTGTTTAA	100
30	AAAAAAAAAA AACAAACAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA	150
	GAAATTTAAT GTTTTCATA ACATGAA	177

(2) INFORMATION FOR SEQ ID :46:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 256 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

44

(xi) SEQUENCE DESCRIPTION: SEQ ID :46:

	ACTGATTCTG CGAAAATACC CCCTTTTAT TAGTGGCATG CTCATTCACT	50
5	TTATCTTAT ATTCAAATAA GTTATTTCGC TTTCACTGTT TTAACAAAAA	100
	AAAAAAAAAA AAAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT	150
	TAATTACACAC GGAAAAACCA AGACAAATTTC ACAACTTCTG GACACAACCA	200
10	TCAACACAGG ACATTTTTT TACAGGCAA TCACTTAAA CAAAAAAGAT	250
	CCCAGA	256

15 (2) INFORMATION FOR SEQ ID :47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

	GAGAAAAGTC NNNNNNNNNNA GGTAAATCTA ACTTTTCTTG CTTATTTCAG	50
	CTATGATCTG AAAGGATGGA AGACACAAAA TGTATGNNTA AGGTATTTT	100
30	AACAAAGATA CATGGTAAA TTACAGCAG TAATGTAAA AAGACTGAGG	150
	AGCAA	155

35 (2) INFORMATION FOR SEQ ID :48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :48:

5	GCTTATTTA CTATATCTAA AGGATAAAGC ACAAAATGAT GAATAAGATA	50
	TTTNACAAA GATACACG	68

(2) INFORMATION FOR SEQ ID :49:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :49:

20	CCTGAAAGCA AAGCCATNNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG	50
	GGCCTAGCTA AATTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA	100
	ATTACAGAAG AGTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC	150
25	TCTGCTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG	200
	AAGTTCCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCC ATGG	244

30 (2) INFORMATION FOR SEQ ID :50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :50:

40	ACTCGNNCAG CGATAGTCGG AGCTCACCAA CAAAAACNCT NNNNCAGAAA	50
----	--	----

46

GGANAAAGNG CCGCCCTACG TGGTACACAC A

81

(2) INFORMATION FOR SEQ ID :51:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :51:

15	GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA	50
	AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAAT	100
	TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT	150
20	TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT	200
	TTATACCAGA AGNATGACCA CTG	223

25 (2) INFORMATION FOR SEQ ID :52:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :52:

35	TATGGTTNT TGTAAAAAAG CTCANNANA AAGGGANNGG CTTAAGAGA	49
----	---	----

40 (2) INFORMATION FOR SEQ ID :53:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs

47

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :53:

	CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA	50
10	TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT	100
	TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA	150
15	TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA	200
	TTCAATAATC AAA	213

(2) INFORMATION FOR SEQ ID :54:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 166 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :54:

30	GGGTGTTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTGTGTG	50
	CGTNNTTGCG TANGGGNNGG GTTNGGCAG GTGTTGCCGG TAGCNAACN	100
35	GTTGGCCCCA TNGCCNGNAT TGNNNCCCN CNNGGAANG GGGGGGNGA	150
	CCNNAGNGGG AAAAAAA	166

(2) INFORMATION FOR SEQ ID :55:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 75 base pairs	

WO 94/01548

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :55:

10	ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT	50
	NGNCGTTGTN GCTGCCAAGC GACAT	75

(2) INFORMATION FOR SEQ ID :56:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :56:

25	AATNNNNNCC TATTTTGAA TTTTTTGAA AAAAGTTCAA TGTTCAAGTTT	50
	TCCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATT CTGTGAAGCA	100
	AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA	150
30	TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A	181

(2) INFORMATION FOR SEQ ID :57:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

49

(xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAAATCACC GTTTTCAGG ATGTTTGATC ACAATACGAA 50
5 GATGACGNNA TCCAATTCA GAACACCACA GGGCACTGGC ACACAGAGGG 100
GATTATTACA GAACCACTGA GATGACATTT 130

(2) INFORMATION FOR SEQ ID :58:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :58:

20 GTNATTTGAGGTCACAAATNTAAAGA CTTATTGTAG CCCATGAACA 50
CATTGACAAG TACAAAAATT ACAAAAATAT GCAGAAATAT TGAATAACTA 100
25 GAAACACAAGC CACTGTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTT 150
CCATGAA 157

(2) INFORMATION FOR SEQ ID :59:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :59:

40 GAGGTGAAGT TGTTCTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC 50

50

CTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAc GNCCACAAAT 100
 GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATT 150
 5 TTGAACAGGG AGGGGAGAAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG 200
 AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA 250
 CA 252

10

(2) INFORMATION FOR SEQ ID :60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC 50
 15 GCCTTAACCTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG 100
 25 AAAGGAAGCA ACAAAATAATG TCGCTTTCA CCTGACGTCT GGTTCAACTT 150
 TCCGCCAGC CTATTCCGN GTCTTCCTCC TGCCCTTCTA ATGTCCCA 198

30

(2) INFORMATION FOR SEQ ID :61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:

51

	GAGGTGGCAT TATGTGAGAC AGCATTGGT TAGGGAGTGC CAAGCATTCT	50
	ACAGCATTG ATGGTGGAAA TAGTCATGCT TTTTATTTCT GCTCTCTAGG	100
5	AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAAGGTC	150
	CAGGTAGAGG CAATTCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA	200
	GAGTGCTTCT CATAACACCTT CAGGAACCC	229

10

(2) INFORMATION FOR SEQ ID :62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :62:

	CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAAA GGGACTGAAG	50
25	AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA	100
	ACCGCTTAAT GAATTCATG ACCTTGAGGG CTAAGATCG TTCTTCGGGC	150
	AAGAGCTTTT GGACTGTTT TAGAACAGAA T	181

30

(2) INFORMATION FOR SEQ ID :63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :63:

WO 94/01548

52

GTTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA

50

ATTTGGCAGA AACAAAGAAAA GGACATGGGA TAACTTTAG ATTTAAAGAG

100

5

GCAGGCTTGG AACACAAACT GGTATTCTGC TGACACACTG CTGCATATCA

150

TAAGGCTACT CCACAAGACC ATTAGAAAGTC

180

(2) INFORMATION FOR SEQ ID :64:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :64:

20

ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC

50

AGGGAACGTG GATTATTAA AAATANGCNA GAACTTATT CANCTGTGCT

100

25

TTAGAAANAA NTGTATACGG

120

(2) INFORMATION FOR SEQ ID :65:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :65:

40

CACATCGCTA TAATCCTTTC TGAGGACTTA AAACTTATN CCACTTACCT

50

TTATGACTTT TAACAAGCCT

70

(2) INFORMATION FOR SEQ ID :66:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :66:

	TTTCGAGCAA AATGTTTACA TTTACATGGA AATAACACACT AAAACAGAAT	50
15	ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG	100
	GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAC	150
	CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN	200
20	TCCACACACC CACACGATT AGGAACTTGG ACATGTTCCCT	240

(2) INFORMATION FOR SEQ ID :67:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :67:

35	GGAAGCACTA CATTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT	50
	TACGATATGC TTAGGTAGGC TTTTAACCTTG CTCCCTCCAAA CAATATCTNT	100
	TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT	150
40	AACCTATTTTC TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG	200

54

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA 250
 TAAG 254

5 (2) INFORMATION FOR SEQ ID :68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAGT GAAAGACTAA CCAAGATTG 50
 ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG 100
 20 TCAACAAATN NNNACAAC TG AGAACCTGGG AATTCCCGCA CGGAAGACAA 150
 GAGATAACCT CTCCAATTAA ACACCGCTAG GNTTCTATNN TA 192

25 (2) INFORMATION FOR SEQ ID :69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNNAAA CAAAAGACAG GAGCAGAGAG GCCTGAGAGC 50
 AGGAGGGCAA TTGATCTCT CCTCACAAAC AGCCCAGGAA AATATACACC 100
 40 CGGGGGGAAG CC 112

(2) INFORMATION FOR SEQ ID :70:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :70:

AAGGGTCTCC AATTTAATCC TTGGGTTGTT TTACCACTTC TTTCGTAAAT	50
15 TTATCAAGAT TTCTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG	100
ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT	150
20 ATCACAAATTG AGAAGATGAT GAATGAAGAT TCGCTTCAA GTTCCAAGGG	200
CAGATTATT CCTTTAACTG ACATTTCCAT GA	232

(2) INFORMATION FOR SEQ ID :71:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :71:

35 CNTGGATCCG NCCTTGTAC GNCCAGGACG NCTGGACCGC AAAATGAATT	50
TTCACTTTTC GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG	100
40 GAACCTTGAA GGAGATCGAC TGAAAGACTA GCGNCCNGT CAGATAAGAT	150
TTAGGGCTGA	160

(2) INFORMATION FOR SEQ ID :72:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :72:

	AAGGAAGACT GGTTGCCAT CCGAGATCAT TAAAAANGNC TGACCCCTAAC	50
15	AATACTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCCTT	100
	CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGGAACT TTGATTCTT	150
	TTTCCTCCC GTCGCAAATT CTATGTTGG AT	182

20

(2) INFORMATION FOR SEQ ID :73:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :73:

	CAAGAGGCAG CTGCCCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG	50
35	ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTTGCCCTNG CACAATAACA	100
	CTGAGAGGAT GATGAGAACCA CNCTTGAAAT GCTTCATNCA CATGGGCAGG	150
	ANAGGCTGCA CAATGAAA	168

40

(2) INFORMATION FOR SEQ ID :74:

57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :74:

10

AACCTTTATT CATCCTCCTN TCCAAGACCT ATGAGAAGGT TCCAGGGCCC	50
AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCCGGGGTT	100
15 GTATACCACA CCCCCGGGCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA	150
ACTAGTTCTT TNTNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC	200
NCTNTCCCTN NAATAAATTN C	221

20

(2) INFORMATION FOR SEQ ID :75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNTTG GGTCATCCGA GATCATTAAA AATGNCTGAC CCTAACATA	50
35 GGCACAAAAA TAAAAACCAA ATAAAAAACC TCCTTANNTT CGAAGTATCT	100
TAGAAAAAAA CAGGGCCTTG AGTTCTG	127

40

(2) INFORMATION FOR SEQ ID :76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs

58

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :76:

	AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAAACCA TTTCAAAACC	50
10	CTCTAATAAG TATTAAATGA AAATAAAATT ATCGAAGAGA AACAAATGACC	100
	ACAAAATTAA TACTACAAA TCATTACTGA GACTCTTGCA TTACAATATT	150
15	TGGAGAGTAG GTGAAGAAAAA TNTAGACCGA	180

(2) INFORMATION FOR SEQ ID :77:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 142 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :77:

	GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTTC	50
30	GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAAACTG	100
	TCACTTTAGC CNCNAACTAC AAGACCNGTT AGACTAGAGA GC	142

35 (2) INFORMATION FOR SEQ ID :78:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 124 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :78:

5	GGCCCTGAGA GCAGGACGGC GAATTGATC TCCTCCTTCA CAAACAGCCC	50
	ANGGAAANTA CACCCCCGGGG AANNCCCCNC NCNNNTAGAA CCNNCAGGNT	100
	CTGNCCCCCC CNNNGNCCCC CCCG	124

10 (2) INFORMATION FOR SEQ ID :79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - 15 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :79:

15	AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTCA	50
	TATAGTCTAA AAGCTAGAAG ACAAGAGTG TATTCGTGG GTGGATGTAT	100
25	NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT	150
	TTAAGNAAAN GCCNTTTAA G	171

30 (2) INFORMATION FOR SEQ ID :80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 98 base pairs
 - (B) TYPE: nucleic acid
 - 35 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :80:

35	CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA	50
----	--	----

WO 94/01548

60

CGACAGTGCC GTGNGGGCAT CATGGCACCT NGACCACGGG CNCCTAAG

98

(2) INFORMATION FOR A-2 ID :81:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

15 CCTCAACAAG TGCGAGACCT CGGGGCGTCCAA. CGA
CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT

CAACATCA

50

100

108

20

(2) INFORMATION FOR SEQ ID :82:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

35

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC
CCT AATTG TAAAGCTTAA TACAGGTTNT GGAAATCATT TAACACCCGA
GAATGTCCCCA TCACAGTCTT CCGTCAAAAT TTAGCCTCAC AACACAACA
AATTCTGCA AATTCTTAAT TCAGAAGGAA

50

100

150

180

40

(2) INFORMATION FOR SEO ID :83:

61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10

GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT	50
CGATGCAGCT GCCATGCGCG CCAGAACATCG CGAAGGCATA CCCTTACGTC	100
GTTGGACGCA TGTAGATG CCTTGAGAC CGCCCAGAGA AGTCCTTGTC	150
CTTCTTAATA AACACCTCCT CGCCAATGCA GACGACCACA ATCACCGTA	199

(2) INFORMATION FOR SEQ ID :84:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30

CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA	50
CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA	100
GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG	150
CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATTT	200
NACNGAATAC AACC	214

40

(2) INFORMATION FOR SEQ ID :85:

62

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10

CCTGGGCAAG CTGAATGTGA AGTTGACCAAG GCTAACTGAG AAGCAAGCCC

50

AGTACCTGGG CATGTCCTGT GATGGCCCT

80

15

(2) INFORMATION FOR SEQ ID :86:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :86:

30

GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC

50

CCTGAAATAAC GCGCTTTCA CTTGCGTGCT CAGAGCTGCC GTCTGAAGGT

100

35

CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT

150

GATTAGTCAG TTTTCATTTA TAAAAAAGCA TGACAGTTA TTACTCTGTT

200

40

TCTTTTAATG

210

(2) INFORMATION FOR SEQ ID :87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

63

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :87:

	CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT	50
	ATTTAAAAAT ACTTTTTTG ATTCA GATTC CGGTATGACT GAAGANGCAA	100
10	CA	102

(2) INFORMATION FOR SEQ ID :88:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 275 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :88:

25	GATAGGC GCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT	50
	ACGGGCAGTG AGAACATTAT CTGTATAACA CGAACTGTGA TTATTTAAA	100
	ATAGCAGAAC TTATCNGTCT GTGCTT TAGA AATAACTGTA TACAGTGTAA	150
30	TAAGTTGAAA AGAACTCAAA ATAAC TAATA CAAATAAGAA CCTACGTATT	200
	AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTA AAAA	250
35	TGACACAAAT TCAAAACACG ATCAT	275

(2) INFORMATION FOR SEQ ID :89:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

	GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACGT GCATTACAAA	50
	TTAATAGTAA TTATGGTTTG GNNGTAAT CGAGTTTCAG AATAAAATNA	100
10	AAAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAAGCT TTTGTTTGT	150
	TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAAGTTA AGAGTTTCC	200
15	TCGTGAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT	250
	GCTGTGTACT CCA	263

(2) INFORMATION FOR SEQ ID :90:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 108 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :90:

30	GCGCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC	50
	CACCACAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCG CGAGGGACCC	100
35	CTTGAGA	108

(2) INFORMATION FOR SEQ ID :91:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 206 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

65

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :91:

	GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT	50
	ATGGCTTG G CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA	100
10	TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTCAG AGCACCCACAG	150
	GGCACTGTGT ACACATGAGG GGTTACCTTA CAGAGCCACT GAGAATATAT	200
15	TAATAA	206

(2) INFORMATION FOR SEQ ID :92:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 210 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

	CCTTGGTGG A GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA	50
30	TGGCTTG GC TGATAGATTT GAAGAGACCT CAATTACGTT TTTCAGGAAT	100
	GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTCAGA GCACCCACAGG	150
35	GCACGTGTGA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT	200
	AATAAANNNNG	210

(2) INFORMATION FOR SEQ ID :93:

40

(i) SEQUENCE CHARACTERISTICS:

- | |
|----------------------------|
| (A) LENGTH: 189 base pairs |
|----------------------------|

WO 94/01548

66

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :93:

	AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAAACT AACCTAAAAG	50
10	GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA	100
	AACATGGCGA AAGGAGCTCT CTCTTCCCC GCAGTCTACC AAGCTCCGT	150
15	GCATTTCAC CACATAGATC TGCTAGCTTA CAAATGATG	189

(2) INFORMATION FOR SEQ ID :94:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 160 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :94:

	GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTTGTAA ACTAACCAAG	50
30	CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC	100
	TCAACGCATG ACAAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN	150
35	GTCATTTAAT	160

(2) INFORMATION FOR SEQ ID :95:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 171 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

TGCTTTATAC ATNATNAAAG GTAGGCAC TT CATAAAATT GCATTTGGT	50
AAAAGGCAAC AATTTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTT	100
10 AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTT	150
TAAGGAAACT ACAGAAGGGA T	171

15 (2) INFORMATION FOR SEQ ID :96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT	50
TTCCCCAACC TTTTTATTG CGAAGAAACT CCAGTTGTTA ACTTTTGAG	100
30 AGTTTTTTT GGCAAAAGAA CTNCATTAN C	131

(2) INFORMATION FOR SEQ ID :97:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

WO 94/01548

68

(xi) SEQUENCE DESCRIPTION: SEQ ID :97:

	GTCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA	50
5	GTAAAGTTAA GGCACTGACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA	100
	CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN	150
10	TTACTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGCC	200
	ATAATGTATT GATGATCTGC TGTAACTTG AGAAGCTTCC TGAAGCTCNT	250
15	TTTGAATAAA TTTATNGAAC TTATGAAGA	279

(2) INFORMATION FOR SEQ ID :98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - 20 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :98:

	GTGAGTCTTT CTTCAACTAG GGGATGTTT CCAGGGCACCG CCAGGCCTCA	50
	CTCACGCAGG CCTCCGCGAC AACTGTTCA GACTGACTGA GGATGAAGTG	100
30	AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA	150
	CAAAGCCCC TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT	200
35	GACGAGACCA GGACCCTTA GGATTAAGCA AGTTTATGC GGTCTNAAAA	250
	AACTCCAGGG CCTCCA	266

40 (2) INFORMATION FOR SEQ ID :99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs

69

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

	GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA	50
10	ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTGGT AAAAAATATA	100
	TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA	150
15	GTGCTTACCC CTGGGAAGGG GGTATACGAT GTTGATTTAC TCTTTGGTA	200
	CGTATT	206

(2) INFORMATION FOR SEQ ID :100:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 73 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :100:

30	CGCAACTNTC NCTAACATC CAGTTTCTA ATNTAATAAA AAATGGCAGT	50
	AATTATCCTC ACCTCTCAGG GAA	73

(2) INFORMATION FOR SEQ ID :101:

35	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 108 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

70

(xi) SEQUENCE DESCRIPTION: SEQ ID :101:

5 GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC 50
ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTCTTG ATACTTGAAT 100
15 ACTGCCCG 108
ACTGCCCG

10 (2) INFORMATION FOR SEQ ID :102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :102:

GAATTATCAA ACCATCNTTG CTGACATTAA TTTTCCAGCT TTGATCTTAN 50
NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTCTCA AACGATNTAT 100
25 CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT 150
TCAATATAAC ANAAAAGGN ATTTTGCAAA AAGTACAAGT TTTATGTCTN 200
30 CTGTTAACTG 210

(2) INFORMATION FOR SEQ ID :103:

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :103:

71

CGTAGTCGA TTGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT 50

GTCACCAAAA TTTCTTTCCA AAAAAAA 76

5 (2) INFORMATION FOR SEQ ID :104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

CTTATGATTA ACTAAGCAA TCTTCATAG AAAGATATTA TCAAAGCTGA 50

AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA 100

20 CCGATTGAAT GGTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC 150

AAGTCGCAAG GAACATC 167

25 (2) INFORMATION FOR SEQ ID :105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

TATCTGCATA TCTAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC 50

40 CTCACGGGAC CACCATCATA CAGCAATTG TCATGATCAA AAGAAACATC 100

ATTAGTCGTG CCATAACTGT AT 122

(2) INFORMATION FOR SEQ ID :106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :106:

GAATTCTTCA CTCCAGATT CCAATGCCAA GATACATTGA TACTGAACAT	50
GGAGGCAACC AGGCCCGTTT CCTCCTTCA AAGTCACCC TCACAGACTC	100
ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA	150
GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG	200
TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA	250
AATAA	255

25

(2) INFORMATION FOR SEQ ID :107:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :107:

GGACGTGAAT TGGTGGATA TTTACAAAGA AAACTGTTT CTCAAAACAC	50
TGTTCATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA	100
AGAACTTGCA TTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT	150

73

AGCACTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTCCCT	200
ATACCAAGAN ACANTTATGT GGTAAAT	227

5 (2) INFORMATION FOR SEQ ID :108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GAAAAATNGC ATGAAAGAAG ACTCTNNNN NGCCATACCA TGGTACAATA	50
ATCATNAAA NACAANAACA AAAACAAACA CATAAAACCA CTCACATATA	100
20 CATGTAGATA CAACAAACNAT ATAATATCAA TAAAAAAAAA ATAGNAAAAA	150
AAAAAAAAATAA CA	162

25 (2) INFORMATION FOR SEQ ID :109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCCTATTAA AAGCCCATAA	50
AAATAAAAAA CGAAACCCGA GAACCAAAAT GAACGAAAAT CTTTCGCTTC	100
40 ATTCAATCGTC CCCACAATNC CAGGCCTACC CCCCATACTG ATCATTCAATT	150

74

154

GTTT

(2) INFORMATION FOR SEQ ID :110:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :110:

15	ATGTGCCAAG TAAAAAAATCA ATTNGTNGCC TTTTTCCATT NCGCGGACAC	50
	CCATAGGCAC CAAAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG	100
	AATAAGCTAT GGAAACARGG AATGCTCAA GTGTCCCAGT CTTTCTCCTT	150
20	GCACTCCTTG TTAATAACAA TACACTATAT CA	182

(2) INFORMATION FOR SEQ ID :111:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :111:

35	GAAGGTGAGA ATAGGGTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA	50
	CNTCAAAACC AATGGTAGAA CATCACATT CAAACTGCAA ACCA	94

(2) INFORMATION FOR SEQ ID :112:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 base pairs

75

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :112:

10	TAGGGCAGTG AACACCTAAC TGCCTGATGC TATAANTGAN TGAATTACAT	50
	GNTCATTNGT TAAATTTGT TCTAAACCCA TTAGGAAATT GT	92

(2) INFORMATION FOR SEQ ID :113:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25	GATTGTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG	50
	TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG	100
	ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGAACTCCAA GAATCTAGAG	150
30	GG	152

(2) INFORMATION FOR SEQ ID :114:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 182 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :114:

	TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTTCAGTG	50
5	TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG	100
	GCAGAAGGAG GCTGAGAAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA	150
	TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA	182

10 (2) INFORMATION FOR SEQ ID :115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :115:

	GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC	50
25	TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATAACNTGGC	100
	AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC	150
	TGCCAGGCATG TCTTCAATAT GAGGAAGGCA NT	182

30 (2) INFORMATION FOR SEQ ID :116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :116:

77

	GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTG ATAAANTAAC	50
	ATACAAAAAT GTACAAACAC ATGAGTAAT AATGTAATGA CAAAGGACTA	100
5	TTTCGGAAA AGTGTGTTTT AAAACANNCT AGATTCAGT GCAAAATGT	150
	ACCCCTGGCA CCTCTTAAA CGTAAGAGCA AGCTCAAAAA CACGTAGTGA	200
	TGGAAATAAG CTAGCTACGC TCAATGC	227

10

(2) INFORMATION FOR SEQ ID :117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :117:

	CGAGAGATTG GTAATGAGGA AGCAATTGAG AGGGGNGGAA GCTACAANGA	50
25	NNNNNGGAAT TACAACAATC AGTCTTCAAA TTTTGGACCC ATGAAGGGAG	100
	GAAATTTGG AGGCAGAAGC TCTGGCCCCCT ATGGCGGTGG AGGCCAATAC	150
	TTGCAAAACC ACGAAACCAG GT	172

30

(2) INFORMATION FOR SEQ ID :118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :118:

WO 94/01548

78

	AATGATGGAA GCAATTTGG AGGTGGTGG AGCTACAATG ATTTTGGAAAT	50
	TACAACAATA GTCTTCAAAT NNNGACCCAT GAAGGGAGGA AATTTGGAG	100
5	GCAGAAGCTC TGCCCCTATG NC GTGGAGGC CAATACTTTG CAAAACCACG	150
	AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG	200
	GCAGAAGATT	210

10

(2) INFORMATION FOR SEQ ID :119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :119:

	GGTAAACACA AAGAGTTCT GATAGTGTCT GCACAACAGC AAACCAACAT	50
25	TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAAATTGAT TCTGC	95

25

(2) INFORMATION FOR SEQ ID :120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :120:

	GGAGTATTN AANNTTCAA ACTTTATTAC TTAATGAAAC AGTTTCTATA	50
40	TACTGCTTCC AATATACTTT AATCCTTTTT TTCTCGTTAA ATTTTTTTG	100

79

TTGTTCTTCA GTTGAGCTGA GATACTTTA ATTACTTTT ATTAACGTCT	150
TCCAGAAACC GTAACAGG	168

5 (2) INFORMATION FOR SEQ ID :121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

GGAGTATTTA TCTTTCAAAC TCCNTACTNA GTGAAACAGT TTCTATACCA	50
CTGCCTTCCAA TTACTANCTN TTTNTCNGT TAAATTTCN NCTGTTTTC	100
AGTTGAGCTG AGATACTTT AATATNNNGT NACTGCTTCC AGAAACCGTA	150
ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA	200
ATACATACTT CGGTGACNTT ATGCATCATG A	231

(2) INFORMATION FOR SEQ ID :122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :122:

TCTATGGCAT GAATGTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT	50
AGCTGTTCAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG	100

80

ACACCATTGT ACGGTGTACA ATGTCATGGG ATCAGGTGTT CAAACTGATT 150
 GGAATCTTTC TGAAAAGGAT ATGA 174

5 (2) INFORMATION FOR SEQ ID :123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :123:

CTNNACAGGA GAAGNAAGTA ATGATCATTC CCCAAAAATG TTCTGTTATC 50
 AACTGNNTTT ATAAAAAAATC GATTGTGGGT AGAACCCAGAG AAAAGGCACT 100
 20 TAGTAAAGAT ACTACATGAN GAAARANNTC TGCCCTTTGA ATTCTTANGA 150
 AACATNNNTNG NNGAATCAAT 170

25 (2) INFORMATION FOR SEQ ID :124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :124:

AAGTAATGAT CATTCCCCAA AAATGTTCTG TTATCAACTG NNNTTATAAA 50
 AAATCGATTG TGGGTAGAAG CAGAGAAAAG GCACCTAGTA AAGATACTAC 100
 40 ATGANGAAAA ANNTCTGCC TTTGAATTCT TANGAAACAT NNTNGNNGAA 150

81

TCAATNT

157

(2) INFORMATION FOR SEQ ID :125:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :125:

15	CAACTTGAAA TACATTATGA TGTCTGATAT GATTAATAT CATTGAGNAT	50
	CTTGCAAACA AAAAAAGCAA AAAATTAAAT CTCCATATCA ATCTTAAATT	100
	CTTGGCATAT TTACTTCTGG TAAATATTAC TTCTGGCCT TATTCTATAT	150
20	GTTGTTATTGA AATTGTGTT	169

(2) INFORMATION FOR SEQ ID :126:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :126:

35	GTTCNGTTNN NNNNTGTTCC ACCTTTGTT GAATTTAGT TGTTAGGCTG	50
	AACCTCCGAG CAGTTTNAGG ACTTGCCTGA GTTTTTCTTC	90

(2) INFORMATION FOR SEQ ID :127:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs

82

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :127:

TTTAGTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG	50
AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTCAG CAACTTGACA	100
TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTT TATGCTAAGT	150
15 AGGAAAACCA	160

(2) INFORMATION FOR SEQ ID :128:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 150 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :128:

30	GCCCCACAAC TACATCCTCA TTATTGGCGC CTACAAACTC AACTACGAAC	50
	ACACTCACAG TCGCATCATA ATCTTTGAG GACTTCAAAC TTACTCGGCT	100
	ACCGCTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC	150

35 (2) INFORMATION FOR SEQ ID :129:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 182 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :129:

	AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNNG NTTCCGAAG	50
5	CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA	100
	GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA	150
10	TGAAAAAACCC AAAACACTTA CGANGCTAAT CC	182

(2) INFORMATION FOR SEQ ID :130:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 219 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :130:	
	GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT	50

25	TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC	100
	TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT	150
30	TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA	200
	TGCTTACTTC AAGAAGAAG	219

(2) INFORMATION FOR SEQ ID :131:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 181 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

84

(xi) SEQUENCE DESCRIPTION: SEQ ID :131:

5 AATAATTCAAT CCACCTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAAAA 50
GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT 100
CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT 150
AGAACATCGT TAACGGAATC ACAGATATAT C 181
10 (2) INFORMATION FOR SEQ ID :132:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (2) INFORMATION FOR SEQ ID :132:

GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT 50
25 GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG 100
TAGAAGATGN AAACAACCTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG 150
CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC 188
30 (2) INFORMATION FOR SEQ ID :133:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (2) INFORMATION FOR SEQ ID :133:

85

	GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC	50
	TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGACTTCAGT	100
5	CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTCAC AGAAGCTCTG	150
	TGACTTGGTT GTGGAAGAAA TCTGAACGT TGAACTGT TCAAGTTAAC	190

(2) INFORMATION FOR SEQ ID :134:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :134:

20	ACATTACGAT CACTGATAGT TGGTGTGCCA CTGAAACCCA CATTNTGGTC	50
	AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC	100
25	CAGGGTCCAT TTAACTAAGA GGTGGTGATC TCCACGCCAG CCCCAAAGAT	150
	GTCCTCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA	200
	TCTGGGCCAG CATTGCCATT ATTGAGTTA TCTAG	235

- 30 (2) INFORMATION FOR SEQ ID :135:
 (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :135:

WO 94/01548

86

GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT 50
 ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACCA CTACAAAATC 100
 AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG 147
 5

(2) INFORMATION FOR SEQ ID :136:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :136:

GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA 50
 20 CCAAACAATA CACTAATGNT TCACACNTT NCTTTTACTT GNACNTTAAG 100
 NTCCCAN TGA GTCACGGTGA CTTACCCCTAA ACATCTCAAN NGTNNTCTGA 150
 25 CTNAGAATGC GGAGGGAGTC T 171

(2) INFORMATION FOR SEQ ID :137:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :137:

ACATATATGT GGTAGGATAG AGAGATGGNN NNNGTGTATG ACATAGGTGT 50
 40 TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATTG 100

87

TGTTGTGGTA ATATGTGAGG AGTATAAGGCT GTGACTAGTA TGTTGAGTCT 150

GTAAGTAGG 159

5 (2) INFORMATION FOR SEQ ID :138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

CCACCGACTT ACATCCTATN ACNCTTCGCC TAGCAAACCA AAACTACGAC 50

20 NCACTCACAA TCGCTCATAA TCTCTTNAGG ACTTCAAACT NTCTCTNTGA 100

NCCTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCCNNTGTNC 150

TNCGGGAGAA CTCTCTGTGC TGTACCAAGT 179

25 (2) INFORMATION FOR SEQ ID :139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

GACCTGGGAC GTAAATGATG AGACGGGTAC TTGGCGGAC ATGAAGGAAC 50

40 TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG 100

ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAAGA 150

88

AAGGCGATGA CCAGAGCCGC AAGGCNG

177

(2) INFORMATION FOR SEQ ID :140:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :140:

15 GTTTACAACA TTTACATCCT ATGAACTCAT GGATTATAAA ACATTTGTGA

50

CTTATACGT CTNTGTCAGT TA

72

(2) INFORMATION FOR SEQ ID :141:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :141:

30

GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTAA AGTATTTGTT

50

TTAGTACGNA AA

62

26

(2) INFORMATION FOR SEO ID :142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :142:

5	ACCA GTNNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT	50
	GGTCAGCTTC TCTTTCTTTA TCTTTCTTTC TCCTTTTTA AGAAAACGAG	100
	TTAAGTTAA CAGTTTGCA TTACAGG	127

10 (2) INFORMATION FOR SEQ ID :143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
15
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :143:

5	AATATAAAAG ACAGCAGTTT CACATTCAC ATATTTGAAA AACATTCAA	50
	AACCCTCTAA TAAGTATTAA ATGAAAATAA ATTTATCGAA GAGAAACAAT	100
25	GACCACAAAA TTAATACTAC CAAATCATTA CTGAGACTTT TTGCATTACA	150
	ATATTTGGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATT	198

30 (2) INFORMATION FOR SEQ ID :144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
35
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :144:

5	GTTCCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCA GA AACAAATGGA	50
---	---	----

	90	
	AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNTAC CTAAAGCTTG	100
	TTGCCCTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG	150
5	AAACTGCTTT GTATCTGCTT TGNA	174

(2) INFORMATION FOR SEQ ID :145:

- (i) SEQUENCE CHARACTERISTICS:
- | | |
|----|----------------------------|
| 10 | (A) LENGTH: 156 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :145:

	GAGAAATAGT ACTTTAAAAT AAAACTAACCA TGGTTTGATC AGCTTGAAAT	50
20	AAGATTTCATA AAATGTACCT TTTTGATTG TTTTGTTCCTN GAGTTTCGA	100
	TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAAATTA	150
25	TTTTGG	156

(2) INFORMATION FOR SEQ ID :146:

- (i) SEQUENCE CHARACTERISTICS:
- | | |
|----|----------------------------|
| 30 | (A) LENGTH: 151 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :146:

	AAGATTCCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG	50
40	GTTGGAAATT GGCTGTTTG TTAAATATA TCTTTAGTG TGCTTTAAAG	100

91

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT 150

T 151

5 (2) INFORMATION FOR SEQ ID :147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

CTTTATTTT CTTATACAGA TTCAGAGAAG TAAAANNAG TACCAAACTC 50

20 CAGGTAANNT GGTTTGATCT GATCGATTTG GCTGCATACT TTGGTACGT 100

ATAACATTCT AACTTAAA TAGAAATTTT TATATTACAA AACGAGGAAG 150

AAAATTTA AAAGTTAAAG TACTAGC 177

25 (2) INFORMATION FOR SEQ ID :148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

GATTNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT 50

40 TGGAAATTGG CTGTTTGTT AAAATATATC TTTAGTGTG CTTAAAGTA 100

GATAGTATAAC TTTACATTAA TAAAAAAAT CAAATTTGT TCTTTAAT 148

92

(2) INFORMATION FOR SEQ ID :149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCCNNNN	NTGGNATTGA	ATGTTACCTG	TGCCAGAATT	AGAAAAGGGG	50	
15	GTGGAAATT	GGCTGTTTG	TTAAAATATA	TCTTTAGTG	TGCTTTAAG	100
	TAGATAGTAT	ACTTTACATT	TATAAAAAAA	ATCAAATTT	GTTCTTTATT	150
	TTGTGTGTGC	CTGTGATGTT	TTTCTAGAGT	GAATTATACT	ATTGACGTGA	200
20	ATCC					204

(2) INFORMATION FOR SEQ ID :150:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :150:

35	AACATCGAGG	TCGTAAACCC	TATTGTTGAT	ATGGATCTCT	ATGAATAGGA	50
	TTGGCGCTGTT	ATCTCTAGGG	AACCTCACCG	TTGGCAAGTT	ATT	93

(2) INFORMATION FOR SEQ ID :151:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

93

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :151:

	AATCGAGAGA AAAAATGATG ACACGTAGC AATATCGTCG GANTCCACCT	50
10	ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC	100
	CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAAAC CAGGAAGGTG	150
15	T	151

(2) INFORMATION FOR SEQ ID :152:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 109 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :152:

	TCTGAGAGGA ATACTNNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCCT	50
30	CTAAGTAATT CCCGATATTAA GCAAANCANN NANATTAATG TCCCAGTGAA	100
	TGTAGCCTC	109

(2) INFORMATION FOR SEQ ID :153:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 136 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :153:

AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50
5 TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100
AGGAAAAGGG GAAAAAAACC CATAATGGGC CTAAAAA 136

10 (2) INFORMATION FOR SEQ ID :154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :154:

CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCCTT CATNCACTAT 50
CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT 100
25 TCAAGATGAG TATACGCATC TATCATTGGA ATTGTGTCA TAATTTGTAG 150
GGCCTCATTG 160

30 (2) INFORMATION FOR SEQ ID :155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :155:

ACCAAGTNNNN NNNNGTCAAA TAGGGAAATA TAATTCGATC TCTCGAATCA 50

95

	ACTCTCTGGG TCAGCTTCT NCTNTCTTC TATCTTNCT TNTCTCCTTT	100
	TTTTAAGAAA AACGAGTTAA GTCTAACAG TTCTCGCATT ACAGGCTTGT	150
5	GACTTCATGC TTACTGTAAA GTGGAAGTTG AGATATTTA A	191

(2) INFORMATION FOR SEQ ID :156:

- (i) SEQUENCE CHARACTERISTICS:
- | | |
|----|----------------------------|
| 10 | (A) LENGTH: 139 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :156:

20	CAACTGAACG CTTGGTCAG GCTGCTACAA TGGAAGGAAT TGNGGGCNAN	50
	TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATT	100
	GCCCCAAACA AACGTCGCCG ATACTAATAA GTTGCAGTG	139

25 (2) INFORMATION FOR SEQ ID :157:

- (i) SEQUENCE CHARACTERISTICS:
- | | |
|----|----------------------------|
| 30 | (A) LENGTH: 172 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :157:

40	GGTACAGAGC ACTCTGTACC AACACACAGA ATTACTGTGTT CTGCAAATGA	50
	CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNNGC AGGCAATCTT	100
	TCTTTGTGTT ACAAGATACA ACATTTAACCA GTTATTAAAT GTAATCCTGA	150

96

AGCACCCGCA AATTTACCTT TG

172

(2) INFORMATION FOR SEQ ID :158:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :158:

15	GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT	50
	CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGGAAGNGG GGG	93

(2) INFORMATION FOR SEQ ID :159:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :159:

30	GNATTTTTT ATTGATATAT CATACTTGTA CAAACATTG GGAGTNCANG	50
	TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC	100
35	CA	102

(2) INFORMATION FOR SEQ ID :160:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :160:

	GCTTTTNNNN NNNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA	50
	TAGAACAAAT AANNCNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT	100
10	ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT	150
	ACCGTACTCT GCATATGTAC AAATAAATTCA AATATATTAA ATCATTGTA	200
15	GCGGA	205

(2) INFORMATION FOR SEQ ID :161:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 150 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

	AACTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA	50
30	AGTTGTTTC CATATAAAA ANNNNNNTGA TTTTAAAAAA ACTAANNAAC	100
	TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAAGTGG GNCACCAAAA	150

35 (2) INFORMATION FOR SEQ ID :162:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| 40 | (A) LENGTH: 77 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :162:

TATTCAAAAG AAAAACATGG GTAAAAATGA TAGTGTTAAA TCTTGGCTCT	50
GTGTACATAG ATAGATACT GTTACAG	77

(2) INFORMATION FOR SEQ ID :163:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :163:

GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT	50
TTAGTTGAAG AATAAGGCCTT AAGAGAGAGA AAGGAAAAAC CATAATGGCT	100
AACTTAGCAG CACAACACGG TTCTTTATC AAGGCGTNAT CATCATTCT	150
CAAAC TGCTACAGAA ATGTCTTCCA AA	182

(2) INFORMATION FOR SEQ ID :164:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :164:

GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA	50
TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC	100

99

AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT	150
CAGATTCACA GACATTTGCA AAACAGAAGA TG	182

5 (2) INFORMATION FOR SEQ ID :165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT	50
GAGACATATA TACCACCCAA GTTTAACAC CATATCCCAT CGGCTGTTAG	100
20 TGTATATAAA AAGAAATAA	119

(2) INFORMATION FOR SEQ ID :166:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :166:

35 GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTCC AAACACATAG	50
GATCCCATCT CAGGAGCAGG ACCAGTGTTC AGCTAGATTA AACTTCGCTG	100
40 GTGATCTTGT TGATGCATAT AAAGTAATCT GGCAATATATG GTTAAATTCA	150
AGATGTTATG GCAGAAGTGA CTTGTTTGC TCAACAAGCA TTG	193

100

(2) INFORMATION FOR SEQ ID :167:

(i) SEQUENCE CHARACTERISTICS:

- 5
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :167:

GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCCGTAC CCTTGGAGAG	50
15 GGTGTGCTAG GAGGAGTGT TGGCGAATTT GGACACGTAC TAATGTCTCT	100
GAGCCAGTCT GAATCTCTGT GAAGATGCC CAGTGGAGGT GGCTGAAGAT	150
TAAATGGACA GTTTATAAAG TGTTCTGGA CCCGA	185

20

(2) INFORMATION FOR SEQ ID :168:

(i) SEQUENCE CHARACTERISTICS:

- 25
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :168:

GGACAACACA GCACCCATCC ACTACCCATT CAGAATTAT ATAGAATATG	50
35 TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG	100
ATTCCTAGT CTATTATTT GTGTACAGAT CCTCTAACCA CTTAGAAATA	150
ATTTTAAAAA ATA	163

40

(2) INFORMATION FOR SEQ ID :169:

101

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10	AGACAAATTC NNNNTNNNNN NTGCCTGATA ATTCAGATC CCACCGTATA	50
	GCAAAGGGTG AACATGTTT CAACCCTTA ACTTTTACG GTGTTGAAG	100
15	ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTG	150
	CAGATTACA ATTTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC	200
	CT	202

20

(2) INFORMATION FOR SEQ ID :170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :170:

	TCAGGGAACC AAAAAACTGG CTTGCTTGGC ACCCAGGGAC AGTAGCTGTT	50
35	TGGCTCTCCA CCCAATTAAA AAAACAAATC CCTGCCCTTT CCCCCACCCC	100
	ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT	150
	GGTGCCCAAGG GCTGTAAA	168

40

(2) INFORMATION FOR SEQ ID :171:

102

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :171:

10	AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA	50
	GCAATTATG ACACTTACAT TTACAGTCGA CCTTTACTAA CCAGGCAAAC	100
15	TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT	144

(2) INFORMATION FOR SEQ ID :172:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25	(xi) SEQUENCE DESCRIPTION: SEQ ID :172:	
	ACCCACAGNN NNNACCTAGA GGCCCAGCGC CCAGAGAGGC ACGTAGAAAT	50
30	GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A	91

(2) INFORMATION FOR SEQ ID :173:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

103

(xi) SEQUENCE DESCRIPTION: SEQ ID :173:

	GATTTTTAA TGGGTNGCCT CTTTAGCTT GGAATATTAC GTTTACTTTA	50
5	ATCCAAGTCT AGGCCTTTA AAGGGTCCTT AAAATTAAG TTCAGAATGT	100
	GAATCCCTTT GACATCTATT ACAGGTTATA GGACCTTTT GGTGTGATTA	150
	CGGTTTCAA TACGATTGTA TAAATGAAGT TAACTGGCA GAAGTTAAA	200
10	TGGA	204

(2) INFORMATION FOR SEQ ID :174:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 241 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :174:

25	GTAAATTCATCACATCTT TNNTNTGACT TTCAATGCATT TCTCATACAT	50
	TNNNNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTTAA	100
	ACGAAAGGCG GTTCAATTCA TCAACTTGAA ATGACTATTT ATTTTNAGG	150
30	ATTTTTTAGG GGAAGAGTAC CCATTCGTT TATAAAAACA GATGACAAAT	200
	TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G	241

35 (2) INFORMATION FOR SEQ ID :175:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 211 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

104

(xi) SEQUENCE DESCRIPTION: SEQ ID :175:

	GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT	50
5	TCTCGTGATA GAAAACAGAC ACTGACCTTG GGTATAAGTGG GCCTATAAAT	100
	AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC	150
10	TTACAGGTTT CTTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT	200
	TTGGCCCTTT T	211

(2) INFORMATION FOR SEQ ID :176:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :176:

25	AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG	50
	NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN	100
30	TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA	150
	AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTCT GACCTATGAT	200
	AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCCTTATAA ANAAATCCNA	250
35	AT	252

(2) INFORMATION FOR SEQ ID :177:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid

105

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :177:

	GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA	50
10	GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG	100
	TTGCAGCCAA TCTTCTCAA GCAAACCGAC TTCCTAACAA CTNTCTACAT	150
	CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTAAC ACCACAATCA	200
15	TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC	250
	ATCTGAAGAT ACCAGCTTCA AATACTAAT	279

20 (2) INFORMATION FOR SEQ ID :178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :178:

	TATGCCCTGA AATGAAACCT CTAAGTTGA CAAAATACCC ACAAAAACAG	50
	ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTG GTGGGTGGTC	100
35	GTTCTCAATT TATAAAANAA TAAATGACTT TAAAGGAGAA ATAAATTTAT	150
	GTCAGGA	157

40 (2) INFORMATION FOR SEQ ID :179:

- (i) SEQUENCE CHARACTERISTICS:

106

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :179:

10 GATAATGCAA CTTTGACAG GAAAGCGCGA TTTTACTAT

39

(2) INFORMATION FOR SEQ ID :180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :180:

25 GCAAACCTCAA ACTACGGACG CACTCACAAAT CGCTCATAAT CCTCTCTAAG

50

GACTTAAACT CTACTACACT AATACTTTTT GATGACTTCT AACAAAGCCTC

100

GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG

150

30

TACCACCA

157

(2) INFORMATION FOR SEQ ID :181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:

107

	CCATCCAGGC CAAATAAGCN CGGGCTATGC CCNTGTATTG GATTGCCACA	50
	CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC	100
5	ATTCTGGTAA AACTGGAAG ATGACCTAA ATTTGAAGT TGATGATGTG	150
	CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTTT	195

(2) INFORMATION FOR SEQ ID :182:

- 10 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :182:

20 CATGGTCTTA ACCAGTGTC AATGGAAATCA GTGGATAART CCCCAGGTTT 50
GTTTGTCCCTT CAAATGGGAC AATTTGAGGA ATGCTTTAGG CAGAGGACTC 100
25 AGATGACAGA GCGCCAACCA CCCACAATAG AACCTGCTC ATCACA 146

(2) INFORMATION FOR SEQ ID :183:

- 30 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :183:

40 TAGAGGAATA GGGNNNNNGA CGCCCCNAGT TGTAGGGACC GACGGAGGAC 50

(2) INFORMATION FOR SEQ ID :184:

WO 94/01548

108

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :184:

10	ACGNNTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC	50
	AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG	100
15	CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAAAGAT	150
	GTCCCCATAG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA	200
	TCTGGGCCAG CATGCCTCAT CTGATTCAATC TCGCTTCCAT CAATGNGT	248

20 (2) INFORMATION FOR SEQ ID :185:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :185:

	AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGG CACTCAGGCT	50
35	ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTG	100
	AACGTGGCTT TCT	113

40 (2) INFORMATION FOR SEQ ID :186:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 148 base pairs

109

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :186:

10	GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTCC CAGGATCCCG	50
	ATGTCGTCA ATCACTCCGAA CATGACCCTT TTTTCTTCCA ACGATCAACC	100
	ACTNCNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC	148

15 (2) INFORMATION FOR SEQ ID :187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :187:

20	TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCCT NGCCATACCG	50
	TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA	100
30	GCCAACTACA CTCCCCTGC TAAAAAGATG AAAGGACCAA TCAAAAGATTT	150
	AATTAACCA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC	200
35	TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC	248

(2) INFORMATION FOR SEQ ID :188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

WO 94/01548

110

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTCA	50
GTTTAATACA TAAGTGTCCA ATAATAATGT CAACCCCTCCC TCGCCACAGC	100
10 CAATAATTG TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT	146

(2) INFORMATION FOR SEQ ID :189:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :189:

25 ATTTACCACA AGGGACGATT TCCACACCAA CCCCCAAAAT GTCCCCTATG	50
ACGACGAAAT GTGTATTGAA AACAGCTCTG A	81

(2) INFORMATION FOR SEQ ID :190:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :190:

40 AAGTACAGCA TCCTGCTGCA AAAATGATTG TAATGNCTTC TCATATGCAA	50
---	----

111

GAGCAAGAAT TGAAGATGCA CAAACTTCGT TCTGAATTG TGAGCTTCCT 100
GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA 136

5 (2) INFORMATION FOR SEQ ID :191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA 50
ATGGGGCATA CGACTAATAT GTACATATCA AACAAATCAAT TGCCTCCCTGA 100
20 AATCAAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTTAGGCCAA 150
CA 152

25 (2) INFORMATION FOR SEQ ID :192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCCAGGN NGTCTTGAT TGCCTAGTAA GGTAAAGACG ATTTTATAGA 50
ATNAAGGTGA TTCCT 65

40 (2) INFORMATION FOR SEQ ID :193:

112

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :193:

10	AGGACCCAAA CTACCTTATT GCATTGAAG TTTTACTTAT NCTATTATAA	50
	TCTAAGAGCC CACCCAACAA GGCAC TACAC ATAGATGCTC A CACTCTATA	100
15	GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG	150
	CTGTCAATGA CTAGGGAAAG CTTTTAAGA CCCAGCGATC ATGCAATGGC	200
	TCAACCATGG CGAACATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA	249

20 (2) INFORMATION FOR SEQ ID :194:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :194:

	GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG	50
35	TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC	100
	GCTGCATATG TGACTGTCA GAGATCCTAC TAGATGATCC TGACTAGAAT	150
	GATAATTAAA AGTATTACT TCGAAGCACC ATTTGAATGN TCAT	194

40 (2) INFORMATION FOR SEQ ID :195:

113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :195:

10

GTGATTTAG TTTAAGGATA AGAACCCACT ATATCAACGT CGGGGGGGTA	50
TTTAAGTCAC ACACATAGTT AACAAACNCNC GTNGCGTGCA ATAAATACCA	100
CATCCTTNA TATGNNCNGN A	121

15

(2) INFORMATION FOR SEQ ID :196:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :196:

30

GGGCTTCNNN NNNNNNCATG TGCACTTAGA ACCGTTACTA ACCGAAACAC	50
CATTTGCTTG TCAACAATGT ACCCCTTGACA GCAGGGAGAA ACTTCTTTAT	100
AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAA	150
TTGTGACCAC AAGTCTTGTT TCTTG	175

35

(2) INFORMATION FOR SEQ ID :197:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

114

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :197:

	ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG	50
	AATCAGAGGT ATCAATGAAA TGAGCCAAA GGTTCGAAAG CTCGCAACTT	100
10	CTTCACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT	150
	ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA	200
15	AATGACTAAT CTACAAGCNT GTTATGCCAA ATAATAAGA AACGACTTGC	250
	TTACAGATGC NTTTTAATTG TGG	273

20 (2) INFORMATION FOR SEQ ID :198:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 56 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :198:

30	GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT	50
	GNATATA	56

35 (2) INFORMATION FOR SEQ ID :199:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 132 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :199:

5	GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG	50
	GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTAAC CAACTCTTAC	100
	CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA	132

10 (2) INFORMATION FOR SEQ ID :200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - 15 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :200:

25	AAACTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATAC	50
	GACATTTCAA TCGNACACAA ANTTAAAAAA TAAAACAAAT TTTAAAAAAC	100
	CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTTCCAAC TTAAAATTCA	150
	GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG	200
30	CTGNTACATA CGNCCCACCA GTTCACAAC AATGACACAA CACTACATGN	250
	TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT	284

35 (2) INFORMATION FOR SEQ ID :201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 base pairs
 - (B) TYPE: nucleic acid
 - 40 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

116

(xi) SEQUENCE DESCRIPTION: SEQ ID :201:

	CCTGACACCA ATTCGCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA	50
5	AGTCGGTGCCTGCTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTNT	100
	CTTGNT	106

(2) INFORMATION FOR SEQ ID :202:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :202:

20	CTTTGGAAAA CAAACATTN TTATTACTGA AATAGCAAAA ATCATTCTAC	50
	ACTCCTCCTA AGCATGTTCA ATTAGCATAAC ATTCCAACAA TGCATGAAAA	100
25	AATTNCTAGC CAGAGGCATT TAAGTGATTT CTTCCTAAGT GTTGCTAAT	150
	TCAATGCCAA GAACTATGAT GTTTATCNNT CTGATGGACA AATCAAGAAA	200
	CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT	250
30	CATTACTCTA ACTGTTAAC	270

(2) INFORMATION FOR SEQ ID :203:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

117

(xi) SEQUENCE DESCRIPTION: SEQ ID :203:

	AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA	50
5	AGCTTATTGA TTAGGTGATA TTTTATAAC AATTGAAAGG GCAATATCAA	100
	ATAATGACAT ATGAGAATT TTTATTACAT ATTAAAATG ATTTTACTT	150
	TACAAAANNG NAATTGCAA TTA	173
10		

(2) INFORMATION FOR SEQ ID :204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :204:

	CTGCTTCACC ATCCTGGCGT CTACCAACCT GGTGNGGCTG GGTACTGTGN	50
25	ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT	100
	CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT	150
	CATTAACATT ANTT	164

30

(2) INFORMATION FOR SEQ ID :205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG 50
 AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT 99

5 (2) INFORMATION FOR SEQ ID :206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNNNNG GGAATGAGGT TCTACCAC TCAGAAAATTC 50
 ATGCCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT 100
 20 TGGGGTTAGN TGTTCNAA 118

(2) INFORMATION FOR SEQ ID :207:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACACTT AAAAGNCTNC TCACACAGN ATCTTTTAA 50
 TAAAAAATACC TCTTTCNTAA CTCCACTTTA ACTCCCTAAA ACCCATGTCG 100
 40 AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC 150
 GCTATGCATA ATACCCTCAC 170

119

(2) INFORMATION FOR SEQ ID :208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :208:

TTCAATGAAA	TGCTTGTATA	CAATGATATA	ACAAAGAAC	CCTAAGACAA	50	
15	CGAGAACTTC	AACTAAGTGC	ACTCATGCAG	AATCTCTGCG	GGGAGAAATT	100
	TTTCTCGGGG	AAGTAACCCT	GCCTTGAA			129

(2) INFORMATION FOR SEQ ID :209:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :209:

30	CTTGGCGTCA	TTTCTGTAC	TTCTGACAGT	GCCCTCAGAG	TCTGCAGGTG	50
	GATCCTTTT	TGCATGGCAT	TAATTATATG	AGCAGCCTCC	TTCTGACAAT	100
35	CCAAATTTG	GCTCCAGAGT	CATTCTGAA	NNTCTACACT	TANGGNCTTN	150
	AGCN TGCTCA	TTCAAGGTNA	AGGGGAGTTT	TNAAAAAATAT		190

(2) INFORMATION FOR SEQ ID :210:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs

120

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :210:

10	TCATTGAGTC ATCCTTTTG CCTGCTGCTG TAAGGTTTTT TTTCTTCTAG	50
10	TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT	100
	GATGCAGAAC TGTTTCATAT CTAGAAATG	129

15 (2) INFORMATION FOR SEQ ID :211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :211:

30	CTGTAAGGTT TTCTTTCTTC TAAGTAAC TG TATGATCCAG AGCGACCCAG	50
30	CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG	100
30	AAATGGAANC NNNNGNTTN TTCCTTAATG GACCCCCCN GGGGCNGAAT	150
	GG	152

35 (2) INFORMATION FOR SEQ ID :212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

121

(xi) SEQUENCE DESCRIPTION: SEQ ID :212:

	CTTAACCCCTT TGGAAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG	50
5	TCGAAAGATG AAAACAAC TA AGTTCATAAC CCCCTGCCCG CCATTGACCT	100
	CCCTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTTACATC	150
10	NAACTGCTAA GATTGATACA TTNCAGTCT GCAAAT	186

(2) INFORMATION FOR SEQ ID :213:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 152 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :213:

	CTTAAATGCC TGTTGTGATA TCTTCTTAA ACCTGGAGAG ATTGAATCAA	50
25	CCTTCTCTA AAATTCCCTT CCTTTGCCTC CTCCTCTAAC TTTTCCTCCT	100
	TTCNCGCTTT TCCTCAGGCT TTGNNTTCC TCATGCTTTG CTTCACTCTA	150
30	TT	152

(2) INFORMATION FOR SEQ ID :214:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 35 | (A) LENGTH: 290 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

	TCTTCAGGAG AAGGGGCACC ACTGCTTAA AAAACAATAC TCCNTTATAG	50
	ACTTGAAACAT TTGCAGACAT TATGATCTT GCTTCCAACTC CCACCGTATG	100
5	TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTT	150
	ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT	200
	GTTACAGGAA AATAGGCAGA TAATCAGATA TATATATCTA NNNCCGGGAT	250
10	ATTATTCAAT AGTGGAAATG ATGACTACAG CTATACCTCA	290

(2) INFORMATION FOR SEQ ID :215:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :215:

25	GTTTCTTCCA GTACATCCAA GTTTAAAATT ATTAGCGAAA TGGTCCATGT	50
	TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGGAAAGATCT	100
	GAGAGCATGC TGTTTGGACT GTTGATGCAT ATTCAATGATG TAACAGGTCC	150
30	TGGGCCTCAC TTTACCCCAT TCGTAAAATG GGGATAATGT CACCTGCCCTC	200
	TTACCTACCT CAGAGGGATT TGCAGAAGCAA ACTGTTAAC TTCGAAAACG	250
35	ACCATTTACT TTTAGGATAT CAA	273

(2) INFORMATION FOR SEQ ID :216:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

123

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

	ATCTACGGCT AGGGAGAAC AATGTTCTA CATATTATGG GTAGTGAGAA	50
	CATTATCTGT ATAACAGGGA ACTGTGATTA TTTAAAATTA TGCAGAACTT	100
10	ATTCATCTG TGCTTTAG	118

(2) INFORMATION FOR SEQ ID :217:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25	GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAAAGAAGA AAACAAGTCT	50
	ATCACTAATG ACTTATTTTA CTTAGTTCC ATTACGAAA CCCTTTAAA	100
	TACAAGGCAA CATTTCACA GCTGAAAAAT TACAAC TAAA NGNNNTGATT	150
30	TACCACCAAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA	197

(2) INFORMATION FOR SEQ ID :218:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

124

(xi) SEQUENCE DESCRIPTION: SEQ ID :218:

	CTCGCGAGCA CTCGTCCGAG AGGTCCCATA CNNNNNNNCC CAAGCCCCTC	50
5	AAGGGCCTT GCCAATCTNG TCATTTATG CCAAGTCCTC TAAAACGCAC	100
	TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC	150
	TATTTTAGGC TNCNAGGTCA AAATAAA	177
10	(2) INFORMATION FOR SEQ ID :219:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :219:	
	GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA	50

25	GAAACCTANT AGTTCAACAA ATTAAAAGAA AGAAAGAAAA AAAGCAAAG	100
	TNGGTNTCAG GGCTGGAC	118

30	(2) INFORMATION FOR SEQ ID :220:	
----	----------------------------------	--

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 233 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	

40	(xi) SEQUENCE DESCRIPTION: SEQ ID :220:	
	GAGAGCCCAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTT	50

125

	ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAACGTGA	100
	CTTGGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT	150
5	TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN	200
	NGGTTGGNGG AAATATNNNTT TAATCTCAGG CCA	233

(2) INFORMATION FOR SEQ ID :221:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :221:

20	GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA	50
	ACCCCTTCCC TACTCACTAA AGCATTCCCTA GGACACCAAC AATGAGGACA	100
25	GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA	150
	CTCGACCACC CCCATATNCA CTNTTGGGTAA AAAACAAACG CTTAACCTG	200
	TGAGCCTGCC ATTCTTTT ACGTGTTAAT CAATT	235

- 30 (2) INFORMATION FOR SEQ ID :222:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCCCGG 50
CCTTAGGAAT TGANTGAGGA CTTAAATTTC CCCNGAGGGA GAGNAGTGGA 100

5 G

101

(2) INFORMATION FOR SEQ ID :223:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :223:

20 ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC 50
ATGTCGTCAC CATTCCAACC AGAAAATTGNC ACAAATGCTA CTGGTGGGT 100
TGACCAATT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT 150
25 TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACCA CCGACAAATTA 200
ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC 250
CATTCTTGAG ATACCAGCTT C 271

30

(2) INFORMATION FOR SEQ ID :224:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :224:

127

AGTATTATTT	ACTNGGTCA	CTGGGAACCT	TAATGTGATT	TATTTTGACA	50
ATTACTGTGG	CACATGTTA	ATCTGCAGCT	CCTGGCGACT	ACTGTGCTTA	100
5	T				101

(2) INFORMATION FOR SEQ ID :225:

(i) SEQUENCE CHARACTERISTICS:

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :225:

20	TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT	50
	AGGCCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA	100
	GACCCCTGTTA ANTTTGGTGA AAATAACTTT CCANATTCA A	141

25 (2) INFORMATION FOR SEQ ID :226:

(i) SEQUENCE CHARACTERISTICS:

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :226:

ATTTTCTTAT ACTCCTCCCCA CAGATGAGTT CACAAATACA AAAANTGGTG	50
TACATTTATA CTCAGGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTG	100
TTCTGTTATG TGCAGAGTAG ATTATTCAT ATTTACTTGG TATGGAAAGC	150

128

AGAGTACAGG CTCATGGAC AATAATCATT AAACACACAT TATNTTTAAG 200
AAAANGCTGT TNNAAAA 218

5 (2) INFORMATION FOR SEQ ID :227:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAAACTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNNGTGG 50
TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAGG 100
20 CAGTTAATCC TATGGTTGTG TATCACAAACC TTTTATTAGC AATGCCATCT 150
TCGTCTTGCC TCCNCCTAC TTGAATATCC CTTACGGTCA ACANCCCNCG 200
25 GGGTTGGGC 209

(2) INFORMATION FOR SEQ ID :228:

- (i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :228:

TTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT 50
40 ANCATTTCG CCAGAATGGT GTAATGNNA CAGGGGAGGA AAAAAGTTAC 100

129

AGATGTAAAC AATGACACAG TTACATTTT TTTTAAATG GTAAAACCC 150

TTTTACTGG NCNTTCCAGA ANCTTACAG 179

5 (2) INFORMATION FOR SEQ ID :229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCACAAGT TATTGTAGCA GTGAAACAAT 50

GAGGGCATAAC ACTATATNGA AAAAAAAACC TCCTCCCTNA TTCTCACGCC 100

20 AACCAACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTGGTAA

TACACCATCA TAAAGGNTCC TAAATTCACTC TCTA 184

25 (2) INFORMATION FOR SEQ ID :230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAAGT TCAGAACATA ACAGTTAAGA CTCAGTTTC 50

40 TTTTTAGGTT TAGAATTGAG GAGCAAGTAT TGNTATGGTG AGCTGTTTA 100

GTGCAAACAT TGTTGAGTAT GTTGTCAAAC GTCTAAAAAA 140

130

(2) INFORMATION FOR SEQ ID :231:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTTTNT NNGTTGGGGG CCGTCCCCT	50
15 CCTAAGGCAG GAAGATGGTG GCNNNTNNNG ACGAAAAAGT CGCTGGNGNN	100
NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG	150
GGGGTAAAAG NAANATNNGA ANATGGAT	178

20

(2) INFORMATION FOR SEQ ID :232:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAAA AAACNCNTAC	50
35 CGTCGTCNTA ATACNNANTC TTCCCATAACA AAAATCGTCC NTNTAAATNT	100
NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATT TATANCTCN	150
NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCAATNACC CGGATNGAGG	200
40 GCAACCANGG	210

131

(2) INFORMATION FOR SEQ ID :233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :233:

	ACTGTGCGAG TAGCTTAAA ANNNNNNNN NNACTCAGTT TNATTTATA	50
15	AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC	100
	CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG	150
20	ACTNTCTNAC NTTCAACNA NTATTCACG TAAAAAACAT CACAGTGC	200
	AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCCCG	247

(2) INFORMATION FOR SEQ ID :234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :234:

35	AAACACCAAA NAAANNNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT	50
	GTGGACATTG GAATGTTTAC TGTTATTCTG TGTAGAAAA CAACTNACAA	100
	AAAAGAAAAA TGGNCAACAA AATTGTTCC CGGCNAGGCT GNAGGAAACC	150
40	NGGGGGAAAN TGCCNGGGC	169

132

(2) INFORMATION FOR SEQ ID :235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :235:

GCANCACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA

50

15

G

51

(2) INFORMATION FOR SEQ ID :236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :236:

CAAGTGTAAA TGCTTGACCC TCTCTNCCTC CCCGANTGAA CTCTCTGATC

50

30

TCAAACTTT TTAGGAAAGC CAGATTTAAA GCAGACGTAC CTAAATNCAA

100

A

101

35

(2) INFORMATION FOR SEQ ID :237:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

133

(xi) SEQUENCE DESCRIPTION: SEQ ID :237:

	CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG	50
5	ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA	100
	CAGTTTCCA GCAGTTTCG TATTTNTTT TATTTACGAA TGCCATACTC	150
10	TGTTTT	156

(2) INFORMATION FOR SEQ ID :238:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 148 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :238:

	GCAGNCTAAT TGTGAATCTA AGAAAACTACT CATAGACATC CCACCCCTAAT	50
25	GATTTTACCT NNAACNTTG TCCTTCATCA TAGAACCTA GCAACATCCA	100
	CCTCCTGTAG CACGAAACGA ATCAAACAAC CCCCTGGATA ACCTCTCA	148

30 (2) INFORMATION FOR SEQ ID :239:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 35 | (A) LENGTH: 258 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :239:

	GAGTTTTAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA	50
--	--	----

134

	AATTTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA	100
	AGCACAAAAT CAGCCCTAC CATGGTATAT TTATCATTGA TACATTACTA	150
5	TCAACTAACGC TCAAGATTT ATTCAAGATTT GACTAGTTT TCCACTAAGG	200
	CCCTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA	250
	TCTTCTCT	258

10

(2) INFORMATION FOR SEQ ID :240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :240:

	GAGCATTATT TGATGCAGAA GTTAAAAAC AATAGACTCA AGAAAGAAAA	50
25	CAAACCAGTG ATTCCCCTTC CTCAGATACT GGGACTAACCA CCTTCACCTG	100
	GTGTTGGAGG GGCCACGGAG CAAGCCAAG CTGAAGAACCA CATTAAAAA	150
	CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTAA AAGAAAACCT	200
30	TGATCAACTG AAAAACCAA TACAGGAGCC ATGCAAGAAC TTTGCCATTG	250
	CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC	300
35	AAGGGTNAAC NTNTTNMAA ANNNGCCNAA NCNNGATTT GNACNCCTT	350
	TNNCATTGGC ATTNANTGAA AAAAGTT	377

40

(2) INFORMATION FOR SEQ ID :241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs

135

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

10	GGNGCACTGN TCCGAGAGCT TTTTTNCTG AAGAATAGCA TCTTTAATGA	50
	GTGTNCTAAT CCTTGTTCATC TGAAGTTTG AAATATATTT CCCAGGGTCA	100
	GAACAATACA GAGA	114

15 (2) INFORMATION FOR SEQ ID :242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :242:

30	CTCAAAATNC TGTGACAAAT TTNNNNNGTC AAGTTGTTNN CCATTAACAA	50
	GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCACGNAACAA	100
	AAAAAANCNA AAGNGGGCCC CC	122

(2) INFORMATION FOR SEQ ID :243:

- 35 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

136

(xi) SEQUENCE DESCRIPTION: SEQ ID :243:

5 GAGAAATGGGA AGCCTCATT TGGGGACAAG AACCTGTACA AGGATTTGTG 50
ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAGC CAGTGCGCAC 100
NTATGATATG CCTCATGATA TTNTTGCATC TGAAGATGGG ACTNTGTACA 150
TTGGNGATGC TCATCCAAAC C 171

10 (2) INFORMATION FOR SEQ ID :244:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :244:

AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT 50
TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAAA GTAAAAACAG 100
GACTTTCAAC TTAATCCAGA CTTCTTAACA GTGTTTACAT GTGAGGGAAA 150
CTCCTTTAAG TAATGCGTAG TGTTTTATTT TTACCATCAT TGGNGACAAA 200
30 AAAAACAAAA ACATAAACAT CTNANGTGAA ATATA 235

(2) INFORMATION FOR SEQ ID :245:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

137

(xi) SEQUENCE DESCRIPTION: SEQ ID :245:

	GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG	50
5	TCTAAGTTAA AAACGCCCTG CCCCCCTTCTC GCAGGCCACC TACACCGTNN	100
	TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCCTGC	150
10	NTNTACNTCT AACCNAAACA TNACNGCCGC CACCTACTCA TGCCCTANTG	200
	CAGCNCACCC T	211

(2) INFORMATION FOR SEQ ID :246:

15. (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :246:

25	GGCTGAGAAT CCTTGAGCTT ACCATTGAT ATTTCTATAT TATTTAAGAA	50
	AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT	100
	ATTTGCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT	150
30	GAACATGGTG GTACCTTAGG NATTCCCTT TNTCNATGAA TATA	194

(2) INFORMATION FOR SEQ ID :247:

35. (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

138

(xi) SEQUENCE DESCRIPTION: SEQ ID :247:

	GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
5	GACTTCAACA GCGACACCCA CTCCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACCTTGTC AAGCTCATT CCTGGTATGA CAACGAATT	150
	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
10	GCCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC	249

(2) INFORMATION FOR SEQ ID :248:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20	GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
	GACTTCAACA GCGACACCCA CTCCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACCTTGTC AAGCTCATT CCTGGTATGA CAACGAATT	150
30	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
	GCCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC	248

35 (2) INFORMATION FOR SEQ ID :249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

139

(xi) SEQUENCE DESCRIPTION: SEQ ID :249:

5	GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTCGCGTTG	50
	GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA	82

(2) INFORMATION FOR SEQ ID :250:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :250:

20	GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG	50
	TNTTGCAAAT CCAGATTTGT TGNCATTACT GATGGGCGCG TGAAACCAGN	100
	GAGAGATGCA CAAGATTTAC AGGCC	125

- 25 (2) INFORMATION FOR SEQ ID :251:
- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :251:

40	GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTACACAGGG	50
	AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAAAGGCCGTTTT	100
	TCTGGGGGAG CGGCCGCCTT TAGTCGACCC	130

140

(2) INFORMATION FOR SEQ ID :252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :252:

	GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA	50
15	AAATNAAGTA CAGGTTTCAG GTATTAAAAA TAAATAAAAGA AAAATCTCGT	100
	TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT	150
	ATAAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGGTTTT	200
20	ATGNGATAAT ATCAGC	216

(2) INFORMATION FOR SEQ ID :253:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :253:

35	GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTTAAAATT	50
	ACANTNNNNNC NNNTNGATTN TTAATNTANG TAATTTCTT CCAAAGAAGN	100
	TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAATA	150
40	TANATAACNGC TTCATNCGTT GGGACCATT AAAAGTAATA TAATNAGCTT	200

141

TTTCAGAAG GATCTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAAT

249

(2) INFORMATION FOR SEQ ID :254:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :254:

15	GACCCCATTC TATATTATNC GTNNNGCGAT TTTTAGCCA CCCTGAAGTT	50
	ATATTTNTAT ACCNAGGCTT CGAATAATCT CATCNGACTN ACCACCCTNG	100
	GAAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG	150
20	CTCCCTGGGN TTCTTG	166

(2) INFORMATION FOR SEQ ID :255:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :255:

35	CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTCAA GAGCATCTGG	50
	AACAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA	100
	AGATTTGCTC GCTGAGAAAAG TCCTTGTGGG AAATCGAAGT TGAGGACTAC	150
40	TTTCAGAATT TGCTCGCTAC ACTACTTGA GGATGCTACT CCCGAGCCCC	200

142

CTTCTNTTGT NACAGACAGC AGA

223

(2) INFORMATION FOR SEQ ID :256:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15	GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT	50
	TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC	100
	TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA	150
20	CAAGTCTGCC CTCAAGGAAG CCATGTTGA TGATGATGCT GACCAGTTTC	200
	CTGACGATCT TTCCCTAGAT CATTCTGACC TGTTGTAGAG TTGTTGAAGG	250
25	AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC	292

(2) INFORMATION FOR SEQ ID :257:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :257:

40	AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT	50
	AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG	100

143

	ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT	150
	GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCCTGACGA	200
5	TCTTCCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT	238

(2) INFORMATION FOR SEQ ID :258:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :258:

20	GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA	50
	GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG	100
	AACCGGCTCC AAGCATTCTG CACAGCACTA ATTTAAA	137

25 (2) INFORMATION FOR SEQ ID :259:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :259:

	GCGCGACTTT TAAGGGATT GCNGTGATGC CTGTTGACCC AGTGCCTTCC	50
	TAGCCGGAA GGGGCTCGGC TGGAGTGNNA AGGCTCAGAA AAATTCGCG	100
40	AAGAAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT	150

144

TTTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTT CGTGTACAT 200
 CGGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C 241

5 (2) INFORMATION FOR SEQ ID :260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

GCGGACTTT AAGGGATTG CNGTGATGCC TGTGACCCA GTGCCTTCCT 50
 AGCCGGGAA GGGGCTCGGC TGGAGTCNNA AAGGCTCAGA AAAATTTGCG 100
 20 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150
 TTTTGGACAG GTGGGGCGGT GACCTTGGTA TGTATTTTC GTGTACATC 200
 25 GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA 248

(2) INFORMATION FOR SEQ ID :261:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :261:

GGATCTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA 50
 40 CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCTACT 100

145

	ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC	150
	ACTTCCAAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGACCCCT	200
5	GATCCCTGGA TAAACAGGAT CATTCAAAG NNGTTTATA	239

(2) INFORMATION FOR SEQ ID :262:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :262:

20	GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTTTGTA AACAGCCATT	50
	GGCCTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG	100
	TAGGNTCAGG CCCCCAGAAC CGCCTGGTA CTCACCGCTA GCA	143

25 (2) INFORMATION FOR SEQ ID :263:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :263:

	GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCTGTAA TACCTCCTCC	50
40	TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC	100
	TAAAAAAAAA TAGCAATCCA GATAGGCTTC GATTTCCCGT GACACTCTGA	150

146

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNAA AATGAAATGT 200
TTGGAACCTT TAGCACAGAT TTGTTGGGA AGACACGGTC TTTTAG 246

5 (2) INFORMATION FOR SEQ ID :264:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATACT 50
CTGTGTTAAA TCGTATGCTT TTTAAAGGTA TTTAAAGATT CAACTAGCTT 100
20 TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTGG 150
ACCTGATCTT GATGTTCTGC TGTTGTNAGT CTTGAAGAGC GTATNTGAT 199

25 (2) INFORMATION FOR SEQ ID :265:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

GGTTTCAATC GTCCATCCAA GATAACAAGAG AACGCATTGC CACTGATGCT 50
TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA 100
40 AACAGCTGC CTTCGTGCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC 150

147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCC CTCACAGG 200

AAAAGTGATT GAAACAAATGG CAAATNTTAC CCTGAACGTGA AGCTG 245

5 (2) INFORMATION FOR SEQ ID :266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGAAATATGT TTCTTCCTT TGAGAATTCA CAAAANGGG 50

TCAAAACAA AGCAATGCTG AAAGCGAACCA TCCATTTNGC CTGCAATTCA 100

20 AGGCGAAAAT CCAAAGGCAT C 121

(2) INFORMATION FOR SEQ ID :267:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :267:

35 GGGTCGCTCT CCCCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTCG 50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACTCG CGTTGTCACTC 100

40 TCCCAGGTTG GTACACCCCC CCCCGTTTC CCCAGCCACA CTCCACGGCC 150

AGGGTGGAGG CAGATGTCT 169

148

(2) INFORMATION FOR SEQ ID :268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :268:

TCGCAGGAGA GGAATTACAT GCTCATCCTA GAAGGGGGGG CTGACTGCAG	50
GTGTTGCTGG GAAGCCTCTC CAGGCCCTGGA GCTGGAGTAC CCGTCCTCAG	100
CACTGCCAGC AGAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT	150
ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAAACA AGTGCTGCCT	200

20

(2) INFORMATION FOR SEQ ID :269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :269:

AGGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG	50
ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTG AACAAATTAC	100
TCCACTATAT TAATATTACAC TACACCACTT ATTCTTTCTT GAATTGTAAC	150
CACTAAGTGT AGT	163

40

(2) INFORMATION FOR SEQ ID :270:

149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :270:

10

TCACACTTCT TATTGCTAG CCTAGATAGC AGCAGCTGGG GAATACGTAG	50
GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAC TTCACCTCACA	100
CCACTTATTC TTTCT	115

15

(2) INFORMATION FOR SEQ ID :271:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :271:

30

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA	50
GGGTNTNTNG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN	100
NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC	150
TGCAGAAATN CCTATGTGAC TCTTATAA	178

35

(2) INFORMATION FOR SEQ ID :272:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

	CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA	50
	GGGTNTNTNG TTATGGGGGA CACTCTACTA CGGGATGCCGT ATGATGNNGN	100
10	NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC	150
	TGCAGAAATN CCTATGTGAC TCTTATAA	178

15 (2) INFORMATION FOR SEQ ID :273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

	CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGGAAGAA GATCAGAACCA	50
	AAAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAAACG	100
30	CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC	135

(2) INFORMATION FOR SEQ ID :274:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

151

(xi) SEQUENCE DESCRIPTION: SEQ ID :274:

	TGTCGAGGAG AAGAAACAC TTGATAACAC CCCCGACAT CGTGGGGCTG	50
5	CTTGTCAACAN GAAAGCACCA TGTTCGCAAT GGATTGCTGC AGGTGCTGCC	100
	GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA	150
10	TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTTGTCCCT CTTCCCTCAT	200
	GACATAGGTG AGCAGTTCC AGTCCCACTC C	231

(2) INFORMATION FOR SEQ ID :275:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25	TCGCAGGAGA AGAAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTC	50
	TCTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA	100
30	GCAGGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNNG	150
	NCGTNCCCCAC CATTGATTGA	170

(2) INFORMATION FOR SEQ ID :276:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

152

(xi) SEQUENCE DESCRIPTION: SEQ ID :276:

	ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA	50
5	ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG	100
	AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC	150
10	CTGAGGGAAA CTAATCTGGA TTCACTCCCT CTGGTTGATA CCCACTCAAA	200
	AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA	250
	ACGAAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT	300
15	AGCGTAGCAT ATTNA	315

(2) INFORMATION FOR SEQ ID :277:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 209 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :277:

	ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTGAGA TTTCACAAAGC	50
30	AATGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC	100
	ATAGTTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT	150
35	AGCAGAAATA GGCCCTTCG TGNGCTGTTG TATTTNCTCG GATNGTAGAT	200
	ATAGTAATC	209

(2) INFORMATION FOR SEQ ID :278:

40

- | |
|-------------------------------|
| (i) SEQUENCE CHARACTERISTICS: |
| (A) LENGTH: 107 base pairs |

153

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :278:

10.	AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC	50
	TGCTGTTAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTA	100
	GAGTCTT	107

15 (2) INFORMATION FOR SEQ ID :279:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :279:

20.	ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAAC	50
	CAGTGCAATA GGCTCCAAAA ATGGCTTTA AGACCTTTGG NGGGCAGTT	100
	ACTACTGCTT TAAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG	150
	TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC	200
35.	GTCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCCNCT ATAAGTGCAC	250
	AAAGGGAAA CACTGATTTC AAGCTT	276

40 (2) INFORMATION FOR SEQ ID :280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 base pairs

154

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :280:

	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
10	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
	TAAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATAACA	150
15	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT	185

(2) INFORMATION FOR SEQ ID :281:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 186 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :281:

	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
30	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
	TAAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATAACA	150
35	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA	186

(2) INFORMATION FOR SEQ ID :282:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 198 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |

155

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

	TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTCGAGA GTCCATGTT	50
10	TATAGAAACC TTGAGGTCCG CCAGCCGTGT CTGGCCAAT GAGATGTAGT	100
	TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT	150
	GTAGGCACAG GGAGACTCAA AAGCACGAGT TNTGAAAGCG TAAATGGG	198

15 (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

	AGAAAAAGGT GAAGCGAAGC CCAAGGACAC CATGCTAAGG GCAAAAGTAA	50
30	GAGACAGTCT CAGAACTGAG AGAACATGTGT CTTCTGCTTT TTGAAGTAGA	100
	CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC	150
	CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTGTTG ACAGCTTCT	200
35	CAGCTCCCTG ACTCCGTTA CC	222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

156

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

	ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA	50
	ATGTGNGACG ACACGTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA	100
10	CCTTTGNCGC TGTTTNTGCA ACGTTCCGAG TGN TACTCTG CGTGAACCGG	150
	TAGACTGCTT GG	162

15 (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

	GGATCCANGC AAAGCCC ACT CCTCCAGGGT GAAGTTTTC TCCCGCGACA	50
	GACAGCAGAC TCGAGCC	67

30 (2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :286:

157

	GGTCGGATCA GGTCACCCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA	50
	GGCAGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT	100
5	TCTTGTCCGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA	150
	GAA	153

(2) INFORMATION FOR SEQ ID :287:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :287:

20

	TACTACGGCT AAGGAGAAC AATGTTCTA CATATCACGG GTAGTGAGAA	50
	CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT	100
25	CCATCGTGCT TTAGAAATAA CTGTATACAG TGTTATAAGT TGAAAAGAAC	150
	TCAAAATAAC TGATATAATT ACATCTATGT ATTAGAATTG AAAAAAGCTG	200
	CTTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAAACC	250
30	GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC	293

(2) INFORMATION FOR SEQ ID :288:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

158

(xi) SEQUENCE DESCRIPTION: SEQ ID :288:

	AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT	50
5	CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCC	100
	GTGTTGAATC ACTG	114

(2) INFORMATION FOR SEQ ID :289:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :289:

20	ATGAACCACT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTGCTGGA	50
	AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC	100
25	CAGTGCCACA ACCATGGGGC GCCAACCCACA AGCAGGAGTG CCACTGCCAC	150
	GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC	200
	AGCGTCCGGG AGCCTCCCTG TCCTTGTGTG GGGTATGGNG CTCTGGCGTT	250
30	GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT	290

(2) INFORMATION FOR SEQ ID :290:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

159

(xi) SEQUENCE DESCRIPTION: SEQ ID :290:

10 AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN 50
5 NACTTTGTTG CTTTGCTGAT TTTAACAGCT TGATTCTAAG CNCTTACTAG 100
TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTACTTT TTGCTACTGT 150
15 TTTGTAGAAC GATGTACATG AATGAGGCCT 179

(2) INFORMATION FOR SEQ ID :291:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :291:

TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG 50
25 TGCCATTACC ATCGGCATCT ACTTATTAAAT TATGTCCTGT AACTCTGCTT 100
CTGTGGGATT CTGCCCAAGA GATCTCATTA CAGTTCCCAA TTCTTTGTTG 150
30 TTATAGTACC ATCACCAATT CGTTAAATAG TGAAAGAGCT TTTTGAATC 199

(2) INFORMATION FOR SEQ ID :292:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

GGAAGACCAT TCTGATCATC CTCACTGACG CCPGGCAA GAGGGTGGTT 50
 TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGACTGGA CCTCTGGNCT 100
 5 CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC 150
 AACCGAANNG ATATTACAAT GTAAAAA 177

(2) INFORMATION FOR SEQ ID :293:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :293:

20 ATTGGTTTC CTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA 50
 CCAACCANAG CTTTGGTCCA TACAGCTTC TTCTAGATTN GGAGACTCTC 100
 25 AAGGACAGCA GGNNGTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT 150
 TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAACCTTGN GTCTGTTCT 200
 TTTAGGCTCT TTTTGCAGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC 250
 30 CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GGCCT 295

(2) INFORMATION FOR SEQ ID :294:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

161

(xi) SEQUENCE DESCRIPTION: SEQ ID :294:

AATGATCCTT TTTTCGCTCT TACCTATAAGT ACAAGTCCAT GATACTACTG	50
5 CATATTTAC CATTGGNAA ACTGTGAG	78

(2) INFORMATION FOR SEQ ID :295:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :295:

20 ATTCTGTACC TGTTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATTT	50
GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG	100
GGGAGGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTTGAGA	150
25 GAGCCCGGTA ATA	163

(2) INFORMATION FOR SEQ ID :296:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :296:

40 AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC	50
CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA	100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT 150
CGTGCCGGTG CGCTCCACCG ACACCAACAT GGCCCCTTC 189

5 (2) INFORMATION FOR SEQ ID :297:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCCTGAAC TTCCGTCCC CACTCACACA 50
AGTGGTCCGG TGTCACCCCTG CAGTTGGTA TAGTCATAGG TACCATTTGAT 100
20 GACGCCCTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG 150
GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC 199

25 (2) INFORMATION FOR SEQ ID :298:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCCTT AAACGNTAGG 50
CTCTGGAGAA ACAAGTTGTT CTGTCGAGCC CTTGCCATCA ACACACTAAG 100
40 CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT 150

163

GTATCATCAT GCTGCCTCCT GCATTTGAAT T

181

(2) INFORMATION FOR SEQ ID :299:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :299:

15	AACATTGTTT ATTCAATCCAG CAGTGTGCT CAGCTCCTAC CTCTGTGCCA	50
	GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTTAGC ACAGCCTGGG	100
	GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA	150
20	CTGCAAGCTG CTTGCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT	200
	CATCTGGTTG TGACTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT	250
25	TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAAATGG GATTTTTTCC	300
	GAGGCATGTA CATT	314

(2) INFORMATION FOR SEQ ID :300:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :300:

40	AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC	50
----	--	----

164

	CACGCCAAC A GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT	100
	TTTAAGAACT GCCTAGAAAT CTCGTGAGG CACGAAGGGC TTGAGCCAGA	150
5	AAGGAGAGAC AAGTGCAA	168

(2) INFORMATION FOR SEQ ID :301:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :301:

20	ACCCCACATG CCCAGATGTC CACGNNGCTTG CNATACGCCT CTTTGCAAAG	50
	GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCCTG	100
	CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT	142

25 (2) INFORMATION FOR SEQ ID :302:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :302:

	AGAATT CGTA ACTCAT CCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT	50
	GATGACCAAC AAAGACTGAA GTTCCCTATC TACGGAAAGG CATGACTGGG	100
40	AGGCCACAA GGACTCTCAT TGAGTTCTTA CTTCGTTCA GTCAAGACAA	150

165

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG 197

(2) INFORMATION FOR SEQ ID :303:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :303:

15	AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT	50
	GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC	100
	CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA	150
20	TTCAGATACT CAAAAACGTT TCACTCTGTC TAAATGAAC AATTGAATT	200
	AAAAGTTTTT GAATAAAATGA TGAAAATTTT TAACT	236

25 (2) INFORMATION FOR SEQ ID :304:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 220 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :304:

	ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC	50
	CATGTTCCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG	100
40	TCTAGCACAG CCACCGCCCC CATGCCAGG CTCAGGAGCA CACTGAGGTC	150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT 200
 TTAGGCCTCC CGTACAAACT 220

5 (2) INFORMATION FOR SEQ ID :305:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACACCATTAC CATCCATATT GACATCGCAT TTCCATAGAA 50
 ATGCCAAAGA AAGAAGGTCC TGGGGTTTT TATAGAAGCT CAAAAAGNTC 100
 20 AACCTTCGAT GCTATCCCC AGCCCAATAC AAAATCAGAA AAAGC 145

(2) INFORMATION FOR SEQ ID :306:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :306:

35 AGTCAAGGCA TTATGGTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50
 TNGCTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100
 NGNTGATATA AACAGATNNA 120

40

(2) INFORMATION FOR SEQ ID :307:

167

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :307:

10

AGTCAAGGCA TTATGGTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50
TNGCTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100
NGNTGATATA AACAGATNNA 120

15

(2) INFORMATION FOR SEQ ID :308:

(2) INFORMATION FOR SEQ ID :308:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :308:

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTATCAT 50
AAGATGCCACA CATAAACCTCC ACCGATTAATT AAGATTCGAGC GAGGAGGCTGA 100

30

GGACACCCAG ATGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC 150

— 4 —

TGGCCCTTCCTT GGGGACACGGG AGCCCTATTC AAAANANAGTC ACATCTGAGG 200

AGCCGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG 247

INFORMATION FOR SEQ ID :309:

REOURNCE: CHILDREN'S BOOKS

168

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :309:

AGGTAAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG	50
10 AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACTGTGA TACGTATAAT	100
ATGCGTT	107

15 (2) INFORMATION FOR SEQ ID :310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :310:

GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG	50
30 ATTCTGGGGT CCACCCCTCTC CAGTCAAGAG AACCCCCGTC GGGTTTAATG	100
TATCAGGAAA GAGA	114

(2) INFORMATION FOR SEQ ID :311:

- 35 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

169

(xi) SEQUENCE DESCRIPTION: SEQ ID :311:

	ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCAC	50
5	TCCACTGCCT CCTGGACCCT AGTTTCCTCC ACTATACGGT CCCCCCATGT	100
	TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC	150
10	GCTGGTTATA ATTTCCAAAATATGTAATT CCACCTCCAA ATCCTTATA	200
	GTTGTCAAA CCACCTCCGT AGCCCCCACC CTGTTGC	237

(2) INFORMATION FOR SEQ ID :312:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 147 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :312:

25	TNNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG	50
	TGGTGCAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA	100
30	GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC	147

(2) INFORMATION FOR SEQ ID :313:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 151 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

CACAAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG	50
CAGACAAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA	100
5 CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG	150
G	151

(2) INFORMATION FOR SEQ ID :314:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :314:

20

GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC	50
AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA	100
25 AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT	150
TATCACTAGG CTAAAACCTGG ACAAAAGACCG CAAAAAGATC CTCGAACCGA	200
AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAARTA CAAGGAAGAA	250
30 ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA	287

(2) INFORMATION FOR SEQ ID :315:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

171

(xi) SEQUENCE DESCRIPTION: SEQ ID :315:

	GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT	50
5	GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTCCA	100
	CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT	150
10	GTAAACTAAG GTAGACTACT CTGNGAATAA GAA	183

(2) INFORMATION FOR SEQ ID :316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :316:

	GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTCAG AAAACGTGGG	50
25	TTCTGTGCGT GCAC TGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG	100
	CCACCTTTGC AGCCTGTTTC TGTCAATGTAG TTTCA	135

(2) INFORMATION FOR SEQ ID :317:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :317:

40

	CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC	50
--	--	----

172

	TGCCGAAGTC CAAAAGCTTC AGCATTCCCT TAGTGTCAAG ATCTACTTCA	100
	ATAATNNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC	150
5	CTATNTTTTC TGCGGCTTGA TGGAGATACC TTTACTG	187

(2) INFORMATION FOR SEQ ID :318:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :318:

	TCCCAGGAGA AGGAACCTTG AAATTCATCC CAACGTAGGC TGAGTGACCT	50
20	GAAGAGTTGAC AGACTGCCGA AGTCCAAAAG CTTCAGCATT TCCTTAGTGT	100
	CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA	150
25	ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCAGTGT	200
	GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN	250
	AGCTTTCNGT TGNNNTAA	268

30

(2) INFORMATION FOR SEQ ID :319:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

	ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA	50
	AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGACGGTGA	100
5	GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT	138

(2) INFORMATION FOR SEQ ID :320:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :320:

	AAATGATGAT AAATTCACTCC TCTTCTGCTC TTAAAATTTC ATAAACCTCA	50
20	GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT	100
	GTAATCATAC TTCCCCCA	118

25 (2) INFORMATION FOR SEQ ID :321:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :321:

	AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG	50
	GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC	100
40	GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT	150

174

TTCCCTTTCC

160

(2) INFORMATION FOR SEQ ID :322:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :322:

15	AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAAA CCACCNCCG	50
	AACAGGGCTG CTGATTGTTG CTTTCACTTTG TGNGGTGACC TTGAGCTCCC	100
	TTAAAAAAA AACTTGGAGA ATCACAAC TG GCAATGCACC GCAGTTCTCG	150
20	AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTCC ATATCAACTT	200
	GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAAGTCA	250
25	ACCCCCCTGGG AGTATAATNN TCTCCATANA A	281

(2) INFORMATION FOR SEQ ID :323:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :323:

40	GGAATTTCT CAAAGAAAAAC GCAATAGCCA ATTGGAACCT ACTNTANC	50
	GGC ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG	99

175

(2) INFORMATION FOR SEQ ID :324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :324:

GGAATTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANC	50
5 ANTTTATNNN GTCTTCITTA ANNTAGAGTG ACTTACTGAT TTATTATTGA	100
CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA	150
TTGCCCGCGT TTTTAGG	167

20

(2) INFORMATION FOR SEQ ID :325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :325:

TGATCCAAT CTT CCT GTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA	50
35 AAGACTTTAA AACT CCT AGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG	100
ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCTCTT	150
TCGGGTGCG	160

40

(2) INFORMATION FOR SEQ ID :326:

176

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :326:

10	GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT	50
	GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG	100
15	AACATGAGAG AGCAGAGTGC TCTC	124

(2) INFORMATION FOR SEQ ID :327:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :327:	
	AGCCTAGTTT GAACATCCTC ATCCCGTGT TAGACCGGAT CCGATATAACA	50
30	GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT	100
	CGACAATGTA ACTCTGCAAA TCGATGGAGT CCTTTACCTG CCATCATGGA	150
35	CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG	200
	CTAGCTCAA CAACCACGAG ATCAGAGCTC AGCAAACCTCT CTCTGGACAA	250
	AGT	253

40 (2) INFORMATION FOR SEQ ID :328:

177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :328:

10

GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAA	50
TAGAAGAACG TCAGTATCGG CTCCTCCCAC CATAACCGCG TTNAAAATCGC	100
15 CTCCTGGACC ATAGTTTCTT CCACCATAAG TCCCCCCATG CTCCTGCTAC	150
CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTTAT	200

(2) INFORMATION FOR SEQ ID :329:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :329:

30

TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC	50
TCTTTCTTTT NTCGAAAATN ATAAAATGCA GTATTCTACT TTATATTTAA	100
35 TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG	150
AGCAACAATA GTTCATATGT TCATGTTGC TACTATCACA ATNCAACATA	200
TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTA	250
40 GGATTACCAA CTCACTGCTG CCATGACCGA	280

178

(2) INFORMATION FOR SEQ ID :330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :330:

	CCTGAAAAAC TTTATGGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTNT	50
15	CGAAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA	100
	AATATAACAAG CCCATATTAA CATCGTATTT CTATTAAGAG CAACAATAGT	150
20	TCATATGTTC ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC	200
	AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAAAT	250
	CACTGCTGCC ATGACCGA	268

25 (2) INFORMATION FOR SEQ ID :331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :331:

	TCGCAGGAGA AGGAACCTAT ACACCCTTA TAGAGCTTTA AATCGACTGT	50
	AGAGTTTGTTGT GGTCTTCCAG TCCCCAAATGT TTAATTTCC ATTTGCATTN	100
40	TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC	150

179

TACCATATGC CCTTAAAAAT

170

(2) INFORMATION FOR SEQ ID :332:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :332:

15	TCGCAGGAGA AGGAACCTAT ACACCCTTA TAGAGCTTTA AATCGACTGT	50
	AGAGTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTCC ATTTGCATTN	100
	TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC	150
20	TACCATATGC CCTTAAAAAT NNGGNNNNN NNNNGGNTGA ANGGTTCTGT	200
	GTTCCAAAAA TNTAAGATT GTT	223

25 (2) INFORMATION FOR SEQ ID :333:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :333:

	AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAACTCCCA CAAGTTCTTC	50
	TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTGGCAG	100
40	TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC	132

180

(2) INFORMATION FOR SEQ ID :334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :334:

AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC	50
15 TGGAAATAACC AGTGCCCCAT TCCATCAGAG TCTTTGGCGCG ACTAAAGCCT	100
CCATNTTTGC CAATTCAAT TGTTTGGGAT TCTAGCACTC CTTACCNCGA	150
20 GTAATGCCCT TGCTGCAGAC AACAAACACCT GGACTGNGAG ATGGACCAAT	200
TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT	235

(2) INFORMATION FOR SEQ ID :335:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :335:

35 ATGCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC	50
ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTCA TCAAGTTCGA	100
CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG	150
40 GNGATCACCA ACAGGGAGAG	169

181

(2) INFORMATION FOR SEQ ID :336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- 5 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCGCAC CATCCGCTAC	CCCGATCCCC TCATCAAGGT	GAATGATAACC	50
15 ATTCA GATTG ATTTAGAGAC	TGGCAAGATT ACTGATTCA	TCAAGTTCGA	100
CACTGGTAAC CTGTGTATGG	TGACTGAGGT GCTAACCTAG	GAAGAATTGG	150
20 GNGATCACCA ACAGGAGAGG	CACNCTGNAN TCTTTGGCN	NNG	193

20

(2) INFORMATION FOR SEQ ID :337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT CCACAAGTTC	TTTGTCTAGG ACTTCTAGCT	GCTCAGACCC	50
35 TCAGGGTCTT TGGATTGTTA	CCAAAGTCTG TCAAACAGAC	CAGTAGTTA	100
ATACCTGTAC AGAAAATGT TTCTATTATG	CTTCTAGTAT	CTAGAAATTG	150
40 CTTGCTACAG CATGGAGGTG	GTTCTGCCTT	TCCCTGGCTC	200
CATCTGCAGG ATTCCCAGCT	TTGCTCAGTC	TTCATGCCCA	250

182

AAAGGCAAAC TAAAACGTGTC ATGCAGTGGT AGGTTTGAAGA TNAGCTGCTG 300
CATCATG 307

5 (2) INFORMATION FOR SEQ ID :338:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

AAAAGTCATC CA~~A~~AGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT 50
CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTAA 100
20 TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC 150
TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC 200
25 ATCTGCAGGA TTCCCAGCTT TGCTCAGTCT TCATGCCAC CAGAGGCAAA 250
AAGGCAAAC AAAACTGTCA TGCAGTGGTA GGTTTGAAAT NAGCTGCTGC 300
30 ATCAT 305

(2) INFORMATION FOR SEQ ID :339:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

	AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA	50
	ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG	100
5	G	101

(2) INFORMATION FOR SEQ ID :340:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :340:

20	GTGCAGGAG AAAAAAGTCG TCACGTCA TG CGAGTGCAGA GGGGGCGTGG	50
	AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA	100
	AGGACTTCCC GCA	113

25 (2) INFORMATION FOR SEQ ID :341:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :341:

	ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAT CCAAAGCAAT	50
	ATAAAAGAGC AGAGCTAGGA CTGAACAGAA CATTGGTG TATAACCGGC	100
40	AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA	150

184

ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA 200
TTTCTAGGG 209

5 (2) INFORMATION FOR SEQ ID :342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50
TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100
20 GCTTTTAATC TTCATTTTN NNTTTGTNA TGGTAGGCTG AGATGCTTTT 150
AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTT 200
25 TACCCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC. 250
TA 252

(2) INFORMATION FOR SEQ ID :343:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :343:

40 GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

185

	TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA	100
	GCTTTTAATC TTCATTNTTN NNNTTGTNA TGGTAGGCTG AGATGCTTT	150
5	AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTT	200
	TACCCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC	250
	TACAAAAAC	258

10

(2) INFORMATION FOR SEQ ID :344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :344:

	GAAGGAAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC	50
25	CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG	100
	ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA	150
	TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG	200
30	CACAGGACCC AGGAGTCCGC CCACCTG	227

(2) INFORMATION FOR SEQ ID :345:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 188 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

186

(xi) SEQUENCE DESCRIPTION: SEQ ID :345:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50
5 TAAATGTTGA TTGAATACTA ACAAAAGTAGT GAAAGCAGAC GACACAGTAC 100
CTGGCACACT ACTAAACTGT AAATGTTTC AAATCTGAAT CTGTAGAATT 150
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA 188
10 (2) INFORMATION FOR SEQ ID :346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :346:
AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50

TAAATGTTGA TTGAATACTA ACAAAAGTAGT GAAAGCAGAC GACACAGTAC 100
25 CTGGCACACT ACTAAACTGT AAATGTTTC AAATCTGAAT CTGTAGAATT 150
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT 200
30 NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC 250
TAGAAGTGNA AA 262

35 (2) INFORMATION FOR SEQ ID :347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

187

(xi) SEQUENCE DESCRIPTION: SEQ ID :347:

	CTCTGTTTC CAAACGCCCA TGTGTGCTAT ACTACAAC	TC TTCTCGAGTC	50
5	TGATCAATT TGAGTACCC ATTATAGTTC TTACGACGTT AATAACAAAC		100
	ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTTAAAAGA		150
10	AATNTCTAA		159

(2) INFORMATION FOR SEQ ID :348:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 283 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20			
	(xi) SEQUENCE DESCRIPTION: SEQ ID :348:		
	TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC		50
25	ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGGTCTGATC AATAACATCT		100
	ACAATCGCAC CAATTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC		150
30	CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCTC		200
	TGGGAGCCGT TCGCNCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA		250
35	TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC		283

(2) INFORMATION FOR SEQ ID :349:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 169 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :349:

5 CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AACACNGTGGAA 50
CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC 100
GGGCACGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG 150
10 TGGATCACCC AGGTCAGGA 169

(2) INFORMATION FOR SEQ ID :350:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :350:
25 GAAGNAACCA GTACCAGTCA TCCCCAGAGA TAGATGAAGA CCCGATCCCC 50
AACCCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT 100
GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA 150
30 CTTGGCAACA NCACAGGAAG GGACC 175

(2) INFORMATION FOR SEQ ID :351:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

189

(xi) SEQUENCE DESCRIPTION: SEQ ID :351:

	AAATAAAAAA TAAGNACCA ACCAATGCTA CAGATAATAA GAGCTCAGTA	50
5	AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG	100
	GCACACTACT AACTGTAAAT GTTTAAAAT TGAATCTGTA AAATTTGTAA	150
	GGTTTATGA ATATAATATT ATTAACCTATT ATGTCTCTGA ATTTTNNNN	200
10	NAGGCT	206

(2) INFORMATION FOR SEQ ID :352:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 76 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25	AGACATACTG TAGTGTCTAA ATAATATTTG TCNGAAGATA ACAATTATGG	50
	GACTTTAAAG CCGACAGTGA AATTAT	76

(2) INFORMATION FOR SEQ ID :353:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 245 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40	ACATTTGGCC CTCAGACTGT AATTCACATA CTACTNTGAC TGATACTAGA	50
----	--	----

190
TGACCTGGCT GCCTAGGGC TGTGCTGGTC TGATTTTG TGAGACAAAA 100
ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG 150
5 GGCACCTGCGT TTAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAC 200
GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCCTGAC CACCA 245

(2) INFORMATION FOR SEQ ID :354:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :354:

20 GGAATCTGTG CCACACAGCT GCACACGACT ACTGCCAAA GGACAGCCTC 50
AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG 100
25 CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT 150
CTTGGGTTG AGACTTTCA GNGACAAC 179

(2) INFORMATION FOR SEQ ID :355:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :355:

40 AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCAGTTGC 50

191

TCCAGCATGT TGTCAACCATT TCAACAGAAA TCGCACAAAT GCTACTGTGC	100
AAGGTGCAGC CAATTTNTT GTAAAGTGTGA TTTCTTACG	139

5 (2) INFORMATION FOR SEQ ID :356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

TCCAGGAGAA GGAAAACCTTC CACTTATAAC TGTNTCAGCC TGACTATAAT	50
GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT	100

20 (2) INFORMATION FOR SEQ ID :357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - 25 (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :357:

AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGGAA AGACTAACCA	50
35 AGATTTGGAC ATTGGAATGT TTACTGTTAT TCTTTAAGAA ACAACTACAA	100
AAAGAAAATG TCAACAAATT TTTCTTAGCT AACTGAG	137

40 (2) INFORMATION FOR SEQ ID :358:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 base pairs

192

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :358:

AAGGAACAAG TGGGTCAATT CCACTAAGGC TGCCCTGTCAC TGCAGTCTTG	50
10 ATCAGCTTGT CAATTTGATA CTTCAGCTTT TGGTCCAAGG GACGAAGCTT	100
TTCCAAAACC GTTCAATCT CTACCAAGTCT CAAAACTGCA TCATGTCCCT	150
15 GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG	200
GGNACATGAG CAGCAGCTGN TCTTTAAC	228

(2) INFORMATION FOR SEQ ID :359:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 248 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :359:

30	CAGGAGCAAG GAGGCCATT TGCTGAGCTC TCACAGCTGC TAGAGATGCT	50
	CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTGTT TTTTCTGCCA	100
35	CACTCACCCCT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA	150
	CCAAGAAAAT GAATAAAACA GCCAAACTCG ACCTTCTTAT GCAGAAAATT	200
	GGCATGAGGG GCAAGCCCCAA GGTCAATTGAC CTCACAAGGA ATGAGGCC	248

40

(2) INFORMATION FOR SEQ ID :360:

193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :360:

10

AGGCACCTGT GGAGCCATCC TCCTTGT TTT AATCGTCCTG CTGCTGCTGC	50
CGTTCCGTGT CGCGTCGCC ACATGACCCT GAGGTCGCAA TGATGAGTCC	100
15 TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA	150
CCATGAACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT	200
GNNGGC G T TT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCCAGAT	250
20 GCC	253

(2) INFORMATION FOR SEQ ID :361:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :361:

35

GAGAAC C AG GGCTCCATCC TGGCCTCCTG TN C ACCTTCG AACAGATGCG	50
GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTT	100
CTAACNGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA	150
40 TAAT	154

194

(2) INFORMATION FOR SEQ ID :362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :362:

	GAGAACCAACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG	50
15	GATTAGCAAG CAGGAGCAC A CGAATCAAGC CCCTCCAGCC ACCAAATTTT	100
	CTAACACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA	150
20	TAATCCTGNC CACGCCCT	168

(2) INFORMATION FOR SEQ ID :363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :363:

	AAGGGATAAA AGGAAGCTT GNACCAACTC TACCATCAA NNGGAATTGA	50
35	ACATTCCCAT TAAGGCAGTA AAACAAAAGC CAATAGCAA CATGNATTTC	100
	ATTCAACCAT TGATAGATCT CTGCCGTTAT TCTTCAGTTT CTCTTCTCGT	150
	CTCTCTATTT NTTTCTCTGG TTGTCGACCA GCTGACTNTG NCATCGTT	198

40

(2) INFORMATION FOR SEQ ID :364:

195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10

TTATACAAGT CAAACTTGGA AGGTCAAGT AAGCATAACCT ATGCTGAGAG	50
AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAAGCAAC	100
TCGTACACTT TCAAGTTAA A	121

15

(2) INFORMATION FOR SEQ ID :365:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :365:

30

GGTAAGTTGT ATTTGGGCCA GAATTTAAA GAGCACTATT TCGACATTAA	50
AATGTATTCT TCTCGTATTA ATGCCTACAT CTTCAGAGTT TTCAATGCTT	100
TCTAAAAGTT TCCTCTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC	150
GTTCTTCCTG GCGTCTATAT TTCCTTACA GAGGCAAGGT AGGATTCCGT	200
CTCCAAGGGA G	211

35

(2) INFORMATION FOR SEQ ID :366:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

196

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :366:

	CGGCTACAGC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT	50
10	GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC	100
	ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA	150
15	AAGTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG	200
	ATACAGTGGC CTTCGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT	250
20	TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG	285

(2) INFORMATION FOR SEQ ID :367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :367:

	GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG	50
35	GTCTTGGCAG GCGAACCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA	100
	ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT	149

(2) INFORMATION FOR SEQ ID :368:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs

197

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :368:

GGTTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG	50
10 CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTTGTG CCTCGCTGAG	100
GCAATACTAT AATANGCAAG GAACTTTGA GGCGGAG	137

15 (2) INFORMATION FOR SEQ ID :369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :369:

GCCATCATAA GTTCAAAAGA AAAGAGAAAG TGTATTTCCT CTGTTAGTGA	50
30 CATGTAGTCC CTTTGTTCTA GTAGGAAAAA AGGTGCCTAG AGGTAGTATA	100
TAGAGTAAAT ATTGTTCCCT TGCCTACTCG TGCTTCCAAT GATTAAGGAA	150
ATGTTAAACA NNNGTNAAG TCTGTTTGT CAATGCGGGAA GT	192

35 (2) INFORMATION FOR SEQ ID :370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :370:

5 GAGACTTAAG TAAAACGGCT GCAGGCCAGA TTCGCCACC AGCTCAGAGA 50
5 CCACCTTTAT CCATGCTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT 100
GAAGACCCCTA ACANGCTTT ATGATGGGG TCATATCTAT GGTCACGNAT 150
10 ATAGTAGAAA CCAAAAGAAT GTAAGTATT GTNNATGATT TAAAAAT 197

(2) INFORMATION FOR SEQ ID :371:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :371:

GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATT 50
25 ATACACTCCC GGAGCTGAAA AAACCGAAC A TAAGGGAGTG CACAAGAGCC 100
GGGCTTTGGA GAGG 114

30

(2) INFORMATION FOR SEQ ID :372:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :372:

CTTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCCTCCACA TTCCCTTCAG 50

199

CTCCTAGTTG TTCCACCTTG GCTAACATT TACCAATCTT TTTTTCTATG 100
 AACACGTTCT GCCTTGCTG CTACTTC 127

5 (2) INFORMATION FOR SEQ ID :373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTTC 50
 TTTTCAGTT CTCCTGGTC TGTAACAGGA ATGCCCTTA CTCAGTAGCA 100
 20 GGCGGACACG GCCATGGGTC AAGACACCCCT GCTTCATGGG GAAACCTTGT 150
 TTGTCGTTCC CACCACTGAT TCGGACCCACA TAACCTTATN NNATCCCGAG 200
 25 CGTTAGCAGC AACTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAAGT 250
 TTGGCAT 257

(2) INFORMATION FOR SEQ ID :374:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :374:

40 GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG 50

200

NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT 100
 CCGTGGGAAT CACTGTCTGA GTCTTGTC TAGTATTGAC AGATATAGCT 150
 5 TTGTTCTTGG AGTAGAATTA AGGAATTGCG 180

(2) INFORMATION FOR SEQ ID :375:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :375:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50
 20 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC 100
 TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150
 25 TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAAC ATCTTACTGA 200
 TGCTTACTTC AAGAAGAAGA AGCTGGGAA GCCCAGACAC CAGGAAGGTG 250
 AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA 300
 30 TTGATCAGAA AGCTGTGGAC TTA 323

(2) INFORMATION FOR SEQ ID :376:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

201

(xi) SEQUENCE DESCRIPTION: SEQ ID :376:

	GGGGAATCCC ACCTCACCCA TTGNNGTGAA ATGCTTTTT CTAAGAGGTG	50
5	AAATCACTCG CTGGTGTATA TTTCCGCACA ACCAGAAAAT AGTGNNGGAT	100
	ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTCAGCTT ACATTACAG	150
	ATGGGGGGTA GTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG	200
10	AGTCAGTCCT GCATTTATGT CTT	223

(2) INFORMATION FOR SEQ ID :377:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 122 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :377:

25	GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTCCCC	50
	CAGCCAATCA CTTTAGATGC TGAATCGATT TTAAACANAT GTTTGTCAT	100
	ATGGCTAATC AAGAGCCAGG TA	122

30

(2) INFORMATION FOR SEQ ID :378:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 195 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :378:

202

	GGCAGTGCCT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC	50
	TACAAGGTGG ATAATACTTC GGTACCTTGC TTGCCACAGC CCTGTTCTC	100
5	AAAGCTGAAT TGATAAAATT CTCTTGACT TCCAAGACCT AGCAGTTATA	150
	AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT	195

(2) INFORMATION FOR SEQ ID :379:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :379:

20

	GTAGCCCTGA GGTCATCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG	50
	GGTGACAAAG TTTGACAGTG ATGTTACAA GTCAAACCTG GAAGGTTATA	100
25	GTAAGCATACTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN	150
	GGTTNTNGN AACAAAGCAA CTTGTAATT AAGNTAAAC NGAGCATCAT	200
	ATANNNNNGG	210

30

(2) INFORMATION FOR SEQ ID :380:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :380:

203

	CTGGCTCACCA TGGACAAACCT CAAGGGCACC TTTGCCACAC TGAGTGAGCT	50
	GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA	100
5	ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTACCCCCA	150
	CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG	200
	GCCCACAAAGT ATCACTAAGC TCGCTTCCTT GCTGTTCA	238
10	(2) INFORMATION FOR SEQ ID :381:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :381:

	GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTTAAAGGAA	50
25	ATAGCTGTTCA ACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCACT	100
	CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAAAC	150
	GATTGGAAAT CTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA	200
30	AGCGTCAGCA AAGAGACCCCT CTCTGCACCA ATAAAACAGG TGGAAGAAAA	250
	CCTAGCNCGC ACAGAACATA AGCTC	275

35 (2) INFORMATION FOR SEQ ID :382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

204

(xi) SEQUENCE DESCRIPTION: SEQ ID :382:

5	AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCACCCCCA ACACTTAAA	50
	CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAAGAT AAAACA	96

(2) INFORMATION FOR SEQ ID :383:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :383:

20	GGACTTGATG GCTTCTTC AAGTCATAGA CTTGTGGTAA ACTTCTTGCA	50
	AGGAGCTCTG GGCACCCCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC	100
	TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT	150
25	CAATNCNAAT NGANNGGTTA CTCCAAAGGG ACGAGACATG CACCTG	196

(2) INFORMATION FOR SEQ ID :384:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :384:

40	AAGGAGGCCT TTGAGTCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC	50
	ATTCAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA	100

205

CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG 150

CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT 200

5 CCCCCAT 206

(2) INFORMATION FOR SEQ ID :385:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :385:

GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTCAC 50

20 CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG 100

AAGCCTGGGG NCACCTAGGT GTTTCTATTA TAAA 134

25 (2) INFORMATION FOR SEQ ID :386:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :386:

CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC 50

40 ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA 100

CCAGGACGCC ACGCCGACGA ACAAGGGAG TTCNGAGGAG GAGGAGGCCA 150

206

GGACGAGGCG T

161

(2) INFORMATION FOR SEQ ID :387:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :387:

15	GGTGAGCCTC CGCCATCCAG C	CAAAC TGTGC GAC CGCAGCTGTG	50
	CCGTGGCACG ATGGCGAGGA AGCCAGCCCC AAGGA	CAC TGAAAACACA	100
	ACCAGTCAAT GCCGTGTGGT TTTGTTGAA TATAAATNGC	TGAAAGTGT	150
20	TTTTTTNAG GCAGTAATNT		170

(2) INFORMATION FOR SEQ ID :388:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :388:

35	TCCATCTGAC ATCGCATTC CATAGAAATG GCCAAAGAAA GAACGTCCTG	50
	GGGTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCA	100
	GCCCAATACA AAATACACAG AAAAAGCAAT TATTAACAC GGCTTCGGTT	150
40	TCTTTTTCT CTTTAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC	200

207

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTCA AACTGAAATC 250

(2) INFORMATION FOR SEQ ID :389:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15	GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCCTCC	50
	CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTNA GTACCCTCCT	100
	CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN	150
20	TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTTCCGGGAG	200
	AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC	250
25	GTAGGGCNG AGGGAGGT	268

(2) INFORMATION FOR SEQ ID :390:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :390:

	GTCAGAGCCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA	50
40	GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT	100

208

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAAG CCTAGAGGGG 150
 CCAGGTATAAC ACCTTANAGA GGATGAC 177

5 (2) INFORMATION FOR SEQ ID :391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCTCACAAAAGAG TTCACTGATA 50
 TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG 100
 20 GCAACCCCCAA AAACACCTCT TNCTGNCTGC CTCTGCAA 139

(2) INFORMATION FOR SEQ ID :392:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :392:

35 GAGGAGCTGC CCTCAAGGTC GTGGCTCTGA AGCCTACAAG AAAGTTGCC 50
 TATCTGGGGC GCCTGGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC 100
 AGCCACCCCTG GAGGAGAACAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA 150
 40 AGAAGAACAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGCGGAG 200

209

AAGAAAATTG ACAAAATAATA GAGGTCCCTCA AGCCCACGGA CTCCTGGTCT	250
GAGCCAAT	259

5 (2) INFORMATION FOR SEQ ID :393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTTGGAAAG GTACTGGTCC AATTTATCTA GGAAGTATCT	50
CTTGGAGTTT CAGAAATGCT AGCTTGGACA ACTGAAAAGT CACATCACAG	100
20 CTGGCATTCT GGGGGCTACC AAAACACCCCC TCNNNGAGTA GAAGCTGCTG	150
GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC	189

25 (2) INFORMATION FOR SEQ ID :394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA	50
AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AAACAGA	97

40 (2) INFORMATION FOR SEQ ID :395:

210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :395:

10	AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTC	50
	GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC	100
15	CCCTTGACTG ATTTATTGTC GTCAAAAGCA TGTTCCTCTA TCTTTNNNN	150
	TCAACGATC CGCTGCCTTT CTACATCTGA GAATCTTGTCA AAGCATGGAT	200
	AAACTTGNTT TTATGTTGCA TATTTTNACG GCTTCAACTT GAGT	244

20

(2) INFORMATION FOR SEQ ID :396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :396:

25	TAATATGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT	50
	TTTTATTCTG ATCTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA	100
35	GCTTGCAGT GAAGTATACT AGCAATAATT TTCGTACCTG ATCAAGTTA	150
	TTGCAGCCTT TCTTTCCGT TTCTTTNTG AAGGG	185

40

(2) INFORMATION FOR SEQ ID :397:

211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :397:

10

GGACACATCC ACCCACTGAA CTGGACTGTG	GCCATGACCC AGGGTATCAG	50
CTCCAAACTC TGCCAGGGCT GAGAGACACA	TGAAGGAAGA TGATGGGAGG	100
15 AAAAGCCCAG GAGAAAGTCCA CCAGGGACCA	GCCCAGCCTG TATACTTGCC	150
ACTTACCACC AGGACTCCTT GNTCTGCTCT	GGCAAGAGAC TCTTGTCTGA	200
ACACTGCTTA TCTGACCC		218

20

(2) INFORMATION FOR SEQ ID :398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :398:

GGAAGCAAAA AAACAAAAACT AAGCTCGAAT TTGCTTCCAA ACCTGTAGAT	50
35 TGCATCTAAC CANGTGTCCC TATGCACCTC AGAGTACTGG AATACGAACC	100
CAGCGAGACC TTGTCCCCCTC CCATTTGCT GNACTTTGT TGGTGAAAAT	150
GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATTG GACCCCGAGAA	200
40 AACCCCCAGTA CCTTTNNACCA ATGACCCAAC CANTACCTAC CATCGGCCAG	250

212

(2) INFORMATION FOR SEQ ID :399:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :399:

	TCACTTGATT CATCCGTCGC GGGATTTGGG ACCACTAGCA ACATAATCAA	50
15	CACACTCCTA CAATCTTAGG CTTCACATGT GCTGATGATG ATGAAACCAA	100
	CTCTGCCCA ATCATCTCCC CTTCTNTTAG GGTCTTACTA CATATCGCAA	150
	CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCACTACCC	200
20	TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA	250
	ATAATGAGAT TAAATTTATG TTTCGAGT	278

25 (2) INFORMATION FOR SEQ ID :400:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :400:

	GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA	50
	GCGGGAAGGA ATTAGAGCCT TCTGCTTTG CACCTGCTTT GAGTTAGGAA	100
40	GCAAGCTCTC TTCCCTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTA	150

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA	200
ATGTGTT	207

5 (2) INFORMATION FOR SEQ ID :401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

GAGGCATGGC CACATTCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA	50
GGGGGCCAGC CTGGGGCCTG GGCCTTTAA TCTAAGGACT GGGGAGAACCC	100
20 AAGGGACCTT AGAGGTCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC	150
AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG	200
25 NTTCTCCAAA GATAGCC	217

(2) INFORMATION FOR SEQ ID :402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :402:

TTTACAATAG ATTTCACCTT CANTTAGTC AGAGTTGTTG ATTCAAGACT	50
40 CTTCCCCACAC TCGCACATCG AAACATTTT GTGCCAGGGC TTTGCAGCTC	100

214

CAATTATCTT CTCGACAGCA TATACAGAAT CCCCCACATCT GGAACACTTC	150
TCAGCACCTC CATANNTTGA GCAAATTAG AAGTGTGTTGG ATTTGTGTA	200
5 GGCCTGTGAG GCTGAACACT CTCTG	225

(2) INFORMATION FOR SEQ ID :403:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 95 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :403:

AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG	50
20 ACTGNGGCTT CCACTGCGCC CGTGACNTT ATCGAAGCTA CAGAT	95

(2) INFORMATION FOR SEQ ID :404:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :404:

35 AGGAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG	50
CAAATTCCAA AACAGAAAAG ATTCAACAATN NAAAGGTGCA TACATTAAG	100
40 GGCCACACTG TGTAATACTG TGCCAACTTA TGCGAGTCTC ATTGTTCAAGG	150
ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATAACC	200

215

CCAAATGACT GTAAGCCAGA CTNGAACAT GTCAAAAAG

239

(2) INFORMATION FOR SEQ ID :405:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15	GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA	50
	TGTTCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG	100
20	AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA	150
	GGGATAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC	189

(2) INFORMATION FOR SEQ ID :406:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35	CACCATCCTC CAAGTAAATC CCCCTTAGG AAAGTAAGGG AAAAGACCCC	50
	TTATAGCCCT GAGCTCCCC TTGGA	75

(2) INFORMATION FOR SEQ ID :407:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 190 base pairs

216

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :407:

	TATTCATCCA GCAGTGTGTC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT	50
10	TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT	100
	CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG	150
15	CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC	190

(2) INFORMATION FOR SEQ ID :408:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 194 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :408:

	GAAGACATGG CGCCCTAACAA CTTCGAGACC TGCTGNTAAA TTAAAGCTA	50
30	TTTTTCATTA AACCAACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG	100
	CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG	150
35	CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT	194

(2) INFORMATION FOR SEQ ID :409:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| 40 | (A) LENGTH: 97 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |

217

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGGCCACAAG AGTCATCCAT GGATACAGTT CCAATCATTA TAACCACCTTC	50
TAAAAACAAGA TCATCTTCTG CAGCACCTGG TTTTAGTTA TCCTTGA	97

10

(2) INFORMATION FOR SEQ ID :410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTTGAGCTCC TGGACCCTTC TTTGCCTACA CTGGCCTTCC TCTCGGAGGG	50
ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNNTNTG GTCCAGGGCC	100
AGCTCTTCCG AGGCTCCAGC CTGCTTTCG CCGGTGTCA CAGATCATGC	150
TTTGC	155

30

(2) INFORMATION FOR SEQ ID :411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

218

AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCCTGA	50
AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC	100
5 TCTGCTTCTG TGCTCCCTCC TGAGAACCCCT TTATGAGCCT GATTCCCTCAG	150
TCTCACCAAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA	200
TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT	249

10

(2) INFORMATION FOR SEQ ID :412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :412:

AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCA	50
25 TTTACTCCTC TATAACTCAT CTTCACACCN GCATATTTAA ACAAACTAAC	100
AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT	143

30

(2) INFORMATION FOR SEQ ID :413:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :413:

GGGTCCCCCCC ATTCAAGTAC TCCATCACAA AGTACAGGGCG GTCCATGGTC	50
--	----

219

	TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA	100
	CACCCACTTC TCCACCATAG TGCCTCCAC GTCATCATCT GATCACAAACG	150
5	TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT	200
	GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT	250
	AAAATC	256

10

(2) INFORMATION FOR SEQ ID :414:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :414:

	TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA	50
25	GCAC TGGAAG TTTATCAAAA CCCAGGTGTA AATATGC	87

(2) INFORMATION FOR SEQ ID :415:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :415:

	AGAGGGGGAC CAATCTAACCC ATCGCTCTTC CAGTCCTACC AGCACACTCT	50
40	TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCGCCCCGC	100

220

	GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC	150
	ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG	200
5	CAGTGTCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC	247

(2) INFORMATION FOR SEQ ID :416:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :416:

20	TCTAGCACAC AGCTGGCTC ACAAAAATG CGCGACTTGT TAGAACTAAT	50
	TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA	100
	TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATTT	150
25	ACATTGAAAG GA	162

(2) INFORMATION FOR SEQ ID :417:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :417:

40	CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTAA	50
	GTACTTAGCA AAATATTGT TTNCGTGAT TTAGCTTGTC ATTAACNAA	100

221

GAGCTACTG

109

(2) INFORMATION FOR SEQ ID :418:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 202 base pairs.
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :418:

15	GGATGTAAAT TATATGTTGT TTAAATTTT CCAGCATCTG AAAACCTTAT	50
	CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTT	100
	TAAATAGTAC ATATCATTAA ACCATTCNTT CTAANGTAA GAAGAGCAGA	150
20	AAAAATCTTA TAAGATTATC AGATTTCCCT AATGACACAG AAATGNAAGA	200
	AA	202

25 (2) INFORMATION FOR SEQ ID :419:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :419:

	TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC	50
	ACCACAAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACACG	100
40	CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC	150

222

152

TA

(2) INFORMATION FOR SEQ ID :420:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15	CAGCCCTACA CTCGCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA	50
	TCTACTCGGC CCTCATTCTG CACACCATGA GGTGACAGTC ACGAAGGATA	100
	AGATCAATGC CCTCATTAAA GCAGCCGGTG TAAATGTTGA GCCTTTTGG	150
20	CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT	200
	CTGCAATGTA GGGGCCGG	218

25 (2) INFORMATION FOR SEQ ID :421:

- . (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :421:

35	GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAAACT CCCCCACCCA	50
	GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC	100
40	CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGGCG CTTACTGTGC	150

223

TGCTGGCTGT CCTATGCCAG CCTCACCCAT GTGGGGACCA CGNAAGGCAC	200
ACTCCCTCAC CCCGGTGCCG GGCGTGCAG TCCCCCA	237

5 (2) INFORMATION FOR SEQ ID :422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGGN GTAATA AATACTGCAT CCTTTCCACA ACATAGCAGG AATCTTATAG	50
GGAAATCCAT ATAGTTCTG AACATGTATT NATATACTAA GTCTATATTG	100
20 TTTCTTTACG AAGTGTAAAT AAGTGCTGCA CCATACTGTA AACAAAACTC	150
GAATATTGAC TAAATAAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTCT	200
25 CC	202

(2) INFORMATION FOR SEQ ID :423:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG	50
40 AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCACAAAGTT CAACCTTGA	100

224

150
TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAT
ACTGACTTCG GTTTCTTTT CTCTTCAAAT NCCTATAATN GCTTTACATA 200
5 TTCGTATCAG CACCTA 216

(2) INFORMATION FOR SEQ ID :424:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :424:

50 CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT
100 GCTCGCTGGT CTACTGCCAA AACCCATTTC ACCAACCATTA TGTCCCTCGC
150 CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG
25 GGTGCCCTTT TAAAAAAA 168

(2) INFORMATION FOR SEQ ID :425:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :425:

50 TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGGTTAC
40 TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA 100

225

	GAGGAGTCAC AGTGGAACTT CCCAGCTTA AGATATCTAG CAGAAACTAT	150
	AGCTGAGGAC TAAGGAATT TCAGCCTTGC AGATGTTAA GAAAATAATG	200
5	GCCAGATTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC	250
	TAATTAGG	258

(2) INFORMATION FOR SEQ ID :426:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :426:

20

	TCCACATCAT CTCCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG	50
	CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN	100
25	GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTGAGCAAGCTC	150
	CATGACGAA GGACTTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCACG	200
	CTGAAACTCC AGGGTGGATA ATGCCCGTC AATTTGTGCC AGCTGCTGTT	250
30	CGAATNNNTT TCTTCTCGT AAAGC	275

(2) INFORMATION FOR SEQ ID :427:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

226

(xi) SEQUENCE DESCRIPTION: SEQ ID :427:

	CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA	50
5	GAAGCCGAGA GGCAAAATGT CATCATATGC ATTTNTGGC AAACTGTCGG	100
	GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTT	150
	CTAAGAGTGC TC	162

10

(2) INFORMATION FOR SEQ ID :428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :428:

	ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC	50
25	CCATAGTTCC TGAACTCATC AAAGAACCTTA ACTTCCTGAC GCCAGATATC	100
	TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTAAA	150
	GTCGNNGTTA CAATGATTG NCCTGGACTG AAATTCANGC TGCCTTAAGG	200
30	TGCTGATGAT ATTGAGAAGT	220

(2) INFORMATION FOR SEQ ID :429:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

227

(xi) SEQUENCE DESCRIPTION: SEQ ID :429:

	GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAAGATG GGAGAGGGAA	50
5	GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCTCATGG TGTGATGGCT	100
	GCCCAGGCTG CTCCCTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG	150
10	GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA	185

(2) INFORMATION FOR SEQ ID :430:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 277 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :430:

	GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC	50
25	TACCTGGTCG TGGGAGTAGT GGTCATCGTG GACCCAGGGG TGATCCCTAT	100
	CAACTCTTGG GGTGAGAACG AGCGCATGCA CCTGCCGGAC GCTTCCTGGC	150
30	TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG	200
	GCCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG	250
	GAAGACACCG CAGAGCTCAC TTACCAA	277

35 (2) INFORMATION FOR SEQ ID :431:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 125 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

228

(xi) SEQUENCE DESCRIPTION: SEQ ID :431:

5 AAAGTGCCT TGCGCATCCT GCCAGCCTGC CATGTCTTCA TGCGCTGGTC 50
GAAGGCAGCC NGGACTATGG CCAGGAGGCC AATGTAGTCA CTCAGGAGCT 100
CAGCAAAGGAG GAAGAAGTCA TTGTT 125

10 (2) INFORMATION FOR SEQ ID :432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :432:

GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT 50
TCGAAATAGC ACATTTTTAG CAATAGGCTC TCTACACTAG AGAGCCAGTA 100
25 GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC 150
AATTCCCCCC TTTATAAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT 200
30 ANAANGAAA TGGGGCAGGA CA 222

(2) INFORMATION FOR SEQ ID :433:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :433:

229

	CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT	50
	CGATTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC	100
5	CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT	150
	TGGATCCACT GGTGGAAGGG TTGCCCGCTG GNCAAACGTG TGGTNTAACT	200
	NGNCGTTCC TCT	213

10

(2) INFORMATION FOR SEQ ID :434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :434:

	CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT	50
	CGATTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC	100
	CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT	150
	TGGATCCACT GGTGGAAGGG TTGCCCGCTG GNCAAACGTG TGGTNTAACT	200
30	NGNCGTTCC TCTGCCGGTG T	221

(2) INFORMATION FOR SEQ ID :435:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT 50

5 TAGTATATT TCGTTGTCAG 70

(2) INFORMATION FOR SEQ ID :436:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT 50

20 CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCCGA 100

GACTGATTGA GTACAAAATG AAACTGTGCG TCAGCTTGAT CCATTTGTC 150

25 ACCCTCAAGT AGG 163

(2) INFORMATION FOR SEQ ID :437:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:

TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA 50

40 AGAAGAAACA GAGGACAAAA AACACAGACGT TAAGGAAGAA GATAAATCCA 100

231

ACGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG 150
CTCAGCAACC CCTGAATTG 170

5 (2) INFORMATION FOR SEQ ID :438:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG 50
AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA 100
20 GGGTGGGAAT GGATCAAAGG TGTAAAACA GATCTGTCTC GTAACTGTGT 150
AATCAAGGAA CTAGCACCAAC AACAGGAAGA TAACCCA 187

25 (2) INFORMATION FOR SEQ ID :439:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

AAAAGCAACC AGGTCGAGA AACAAATAGTG TATGTGTTCC TATAGGTATG 50
AGTTATTCAAC TGTAGATTG TTTTCTGCA ATCCTCTGCC GAAATGATNT 100
40 ACACTTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG 150

232

TCGGGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA 200

CTTCCGTAAAA ATGCAAATGT TGAAGATCGN NTCT 234

5 (2) INFORMATION FOR SEQ ID :440:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 203 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTAACTGAG ATAAGTTAG CTTTCCAGTT GACACCAAGT 50

CATCTAGTCT TCCCAGGAGTA GATATAGTTG AGGTACTCCA TTTCCCAAAA 100

20 CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA 150

ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG 200

25 TTC 203

(2) INFORMATION FOR SEQ ID :441:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :441:

GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC 50

40 TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA 100

233

	ACGTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT	150
	GGAATAGGCT TATTAAGTTA CACATTAAA AAGTCATTAG AACATCTCGT	200
5	TCTTGCACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT	250
	GGTT	254

(2) INFORMATION FOR SEQ ID :442:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :442:

20	GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG	50
	CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG	100
25	CAAGGGGCCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC	147

(2) INFORMATION FOR SEQ ID :443:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :443:

40	GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG	50
	CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG	100

234

CAAGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC 150
 TCCGNGNGAG ACGCAGTGGA CTNCGATGNT TAGCNCTAGT NNCCCGCT 198

5 (2) INFORMATION FOR SEQ ID :444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT AGGAGAACAA TGTTCCCTACA TATTATGGGT AGTGAGACAT 50
 TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTC 100
 20 TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA 150
 AATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT 200
 25 TTCTGTGA 208

(2) INFORMATION FOR SEQ ID :445:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGCACATTTC ACTACGGGNT ATGTGCATTC TGGGCTTAGT AATGTCAAAT 50
 40 CACTCTTCTC TCCAGCTTGG CCATTCCTCA TTCCCTTGCGG GCCTGCCCTG 100

235

TAGACCACAG GCTAATGGAA TGTCCGGTC TGNNTCATCA NATTCTGTAA	150
CCTGNAGCCC CCGCTGAG	168

5 (2) INFORMATION FOR SEQ ID :446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCTGATT GGTGGATAAA	50
GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA	100
20 TAACAAACAA CTGATAAAAAT AGCATCAGTC CCTCCACCAG GTTGCCTCA	150
AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA	200
25 CCACCCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA	243

(2) INFORMATION FOR SEQ ID :447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAAAT GATTGCCAC CTGTTTAGA	50
40 AATCTAAAAT NNAAAGTAAC TAAGAGCAA GTGCTATGTG GGTTTTAGAC	100

236

CATGACTGTT TGTGGCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG	150
CTCCTGGGGG AGAGGGATT CAACCCCCCT GATGGCAGGG GGTGCTCTGG	200
5 GGAGGAGAGA GGAGAGAACAA GGCTGTTTG GAAAATATCC ACCACTTGA	250
	251
C	

(2) INFORMATION FOR SEQ ID :448:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :448:

20 ACACTCCAGA NCATCCCAGT AGAAAAACAA TTNNNGCAGGA ACGTGATGGC	50
AACAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAAACATAT	100
25 ACAATNTAGT CTAGAAAAAT AAGTCATTT CATAAAATAA GTTTTTAGAT	150
CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA	200
AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA	250
30 GTG	253

(2) INFORMATION FOR SEQ ID :449:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

237

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

	ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA	50
5	ATACCTCTGT AAGAACGAGA ATACACCATA TGTTATTAC ATGTATAAGGA	100
	GTGATAAGAA AAT	113

(2) INFORMATION FOR SEQ ID :450:

- | | |
|----|-------------------------------|
| 10 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 211 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 15 | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

20	TAGCATCCAG GGGAAAGTTAA TCAATACCGG AAAAATACTG AAATTAAAGA	50
	GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA	100
25	AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG	150
	AAACTATTTG AGATCAAAGT CCTATAAACCA AAGTTAAATG ATTCCAAGAG	200
	GTAAATAGGA G	211

- | | |
|----|----------------------------------|
| 30 | (2) INFORMATION FOR SEQ ID :451: |
| | (i) SEQUENCE CHARACTERISTICS: |

- | | |
|----|----------------------------|
| 35 | (A) LENGTH: 194 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

40	(xi) SEQUENCE DESCRIPTION: SEQ ID :451:
----	---

238

	CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG	50
	NATTCACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTNCTG	100
5	TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTCAAGCA	150
	GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG	194

(2) INFORMATION FOR SEQ ID :452:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :452:

20

	ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA	50
	TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT	100
25	TAAAACTACT TGAATTCTCA CTTCTATAATA GGAGTCAGTC ACTTCTGGGA	150
	CTATAGTGAT GCTTGCAA	168

(2) INFORMATION FOR SEQ ID :453:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 220 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :453:

40

	CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCCAGAC GTGAACCAAT	50
--	--	----

239

TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTTG CCCCCCTTCAC	100
TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACTCCAGA	150
5 TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA	200
TAGGACGCCA GACTACACTG	220

(2) INFORMATION FOR SEQ ID :454:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :454:

20

GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA	50
AGCTCAAAGG TTCTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT	100
25 TGCTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT	150
ATGTAGCATT CTGCTTCAT ATTATCTATT ATGTGTCTCT CTCTCTCAA	200
ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA	250
30 TAGTTTGCT TTGTCTTAG CGGTT	275

(2) INFORMATION FOR SEQ ID :455:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

240

(xi) SEQUENCE DESCRIPTION: SEQ ID :455:

	TCGCAGAAGG AGGAACGGGG ACTTTCCATC CCCTGAACCA AGGCATGTTA	50
5	ACACTTGGCT CCAGCATGTT GTCATCATTC AACCGAGAAAT CGCACAAATG	100
	CTACTGTGCC GGGGTGNAGC CAATTTCTT AAGTAAGTGC TGACTTCCTT	150
10	AACANNTATC TNTNTNTGG CTGTAGGGTG GCTCAGTGGA ATCCATTGG	200
	TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA	250
	TGCTCTNGGG TCTGCCATT	270

15 (2) INFORMATION FOR SEQ ID :456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :456:

	TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC	50
	ACGACCCCTG CGCTGGATAC GGCGACGGTT TCTCATTTCG CCTTTGCCAG	100
30	CTCTCATTCTG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT	150
	TTCTTAAGGA GCAAAACAGC TTCCTTGNNC TTCTTGAGC CTTCAACTTA	200
35	TTTAAACTAC CAAGGAAGTT CAGGAACCTTC CTCAANACGA TGACCTTTAG	250
	ACAT	254

40 (2) INFORMATION FOR SEQ ID :457:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 base pairs

241

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :457:

	ACACTAACTG TTCCATCCGT TATATTTGCT GTGAGGAAAA TTAAGATTCC	50
10	TGTTGTATGG GCTGCACTGT TTCTGGAAGA CTACAGAAAA TCTAACATGG	100
	TTGACACTTC CTGGTAGCCC TTCTGTACAT ACACACACAC AACCAAGAGA	150
15	GAAGACAGAG AGAAAATCCT GGTCCAAAAG ATCACATGAC CTTACTAGTG	200
	TTTCCCCAAT GACTGTAATT TATAAACTAA AAATTG	236

(2) INFORMATION FOR SEQ ID :458:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 108 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :458:

30	GAGANNNNNTT NNGGNAATG NTTNCGCACT GNAGCTAAGA ANAGNNATGG	50
	NNNTAGGGNG NNAGANGNCN TGAACAGAGA AAGCNTGAGG GCTCTGGGAC	100
35	GCTGGTAT	108

(2) INFORMATION FOR SEQ ID :459:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 155 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

242

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :459:

	ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC	50
	CCCACTTCTC CGGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC	100
10	CCATGTTCCCT GCTACCACCA AAGTTCCAC TCTCCATTGG ACCGTAGTTA	150
	GAGGT	155

15 (2) INFORMATION FOR SEQ ID :460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :460:

	TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC	50
	CAACACGCAG TGGCAGTGTG TATTTCTT CTCTTTTTT GTAAATATT	100
30	CTGGTTGTG GAGGTTACA GACATGTGTT AGTATATCCT TGCCTGCATG	150
	TAGTTGTTCA TTACTAGAC	169

35 (2) INFORMATION FOR SEQ ID :461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

243

(xi) SEQUENCE DESCRIPTION: SEQ ID :461:

	ACCNNTGTTTA ATTANTGCCG GGGCTCGCCG TTTGCATACA ATGGCTTACT	50
5	CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT	100
	TTTATCAGCG TACCTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG	150
10	GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT	184

(2) INFORMATION FOR SEQ ID :462:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 275 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :462:	
	AGGAACCNTG TTTAATTANT GCGCGGGCTC GCCGTTGCA TACAATGGCT	50
25	TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA	100
	GCATTTTATC AGCGTACCTT TTTCGCCATG CGCTACCTGC TATTGATGAA	150
30	GGCGGCTTAG GGCAATCGAAA AACCTAAAAG TCGAGCTTNG NNNTGCCGN	200
	AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTGGCCGT	250
	NNACTGNGTT GTTGGCGACA GATGT	275

(2) INFORMATION FOR SEQ ID :463:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 149 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5 AATTCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA 50
ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT 100
GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGGNGCCA GCAATGCTA 149

10 (2) INFORMATION FOR SEQ ID :464;

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID : 464:

ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATT 50
25 CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT 100
GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG 150
CCGAACTCAC ACAGCTAGTG AAGACCAGA 179

30 (2) INFORMATION FOR SEQ ID :465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID : 465:

245

	CTACCTCTGT GCCAGGGCAG CATTTCATA TCCAAGATCA ATTCCCTCTC	50
	TCAGCACAGC CTGGGAGGGG GTCATTGTT TCCTCGTCCA TCAGATCTCA	100
5	GAGGCTCAGA GACTGCAAGC TGCTTGCCCCA AGTCACACAG CTAGTGAAGA	150
	CCAGAG	156

(2) INFORMATION FOR SEQ ID :466:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :466:

20

	ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA	50
	CTGCTGGTTC TGGTTTGGC CACCTCACCC TTGGCCACGT CCCCTCCGGC	100
25	TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCA GGGCCTCACC	150
	ACTCCCCTNT GTCCCCCAG CAGGGGGACA AACAG	186

(2) INFORMATION FOR SEQ ID :467:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :467:

40

	TNNNGATGAN TATANAACCA TCATNGACGG TATTTCCCN NG TCTTGNANTT	50
--	--	----

246

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT

87

(2) INFORMATION FOR SEQ ID :468:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :468:

15	ACTAGAAAGTA CAGCATCCTG CTGCAGAAAT GATTGTAATG GCTTCTCATA	50
	TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTTGCCTGG TATTTGTTGG	100
	AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTT	150
20	AGAGGTCTATA GAAGGTCTATG AAATAGCCTG CAGAAAA	187

(2) INFORMATION FOR SEQ ID :469:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :469:

35	ACGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA	50
	GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAG TTCAACCTTT	100
	GATGCTATCC CCCAGCCCCA TACAAAATAC ACAGAAAAAG CAATTATCAA	150
40	ACATCGGCTT CGTTTCTTT TCNCCTTGAA ATNTTAATGT TTACATACTA	200

247

GTGTGCAGCA CCTACTTCTT NATGCCGTG AACTGAAATC TAGATTTAA 250

ACTGAA 256

5 (2) INFORMATION FOR SEQ ID :470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

CTCAAAACGA CAATTCTGTG CCTGGGGAT CTGACCTGGT GAGGTAGCCT 50

GAAGTCTGAA TGGAGCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA 100

20 GAGGGTTTG 109

(2) INFORMATION FOR SEQ ID :471:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35 GCGGCAGTAT ACAGAACCCA TATCAGTTGG GAAAAACTTT ATCAATCATA 50

GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTGCG TTGNAGACCT 100

40 ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTCT 139

(2) INFORMATION FOR SEQ ID :472:

248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :472:

10

TCGCAGGAGA AGGAATGTT CCAATAGGAA CGCCTGTAGA CTGTTAGAA	50
GAAATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTG	100
15 GCTCTGAGGA CTATAGATTG ATCCTCTAGG TGATGAGGGG CTATTAACGG	150
CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTACGT	200
20 GGCAGTAGAG GATAGAGGTG TTTGGAAGCG CTGGGCAGTT GCAAGCTATA	250
TGGGAGACAT TT	262

(2) INFORMATION FOR SEQ ID :473:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :473:

35

ACAGAAGGAC TTTGTCTCTT TAGCTTGTAA AGCTCAATGA ACATTATCTC	50
GGCAAATGAC TCTGCTTCT CGAAGGTCT TCTCCGCTCC AGGTTTACTT	100
40 GCATCTCTCA TACTNNNTAC AGCCAACATG AACACTCTAT GTATTTCTA	150
AGCTTTCNTC TGTTCAAGAA CTTTGAATTT AAAACGTCT	189

249

(2) INFORMATION FOR SEQ ID :474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA GCAAACCTAA ACTCGAACGC ACGTAATAGT GCTCATAATT	50
CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTGTA TGACTCTAGC	100
AGCCTCGCTA ACCTAGTTA CCCCACTGTC CCCACCGGCG AACTNTTTGT	150
GTTAGTACGC GNGTAA	166

20

(2) INFORMATION FOR SEQ ID :475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTA GTAACACTAA AGAGCTGTAAGAACATTGA AGGTGGTCAT	50
TCCTTCAAAAA CTGTGTTTG ACCACACAAG GTGGGCATTA ACAAACAAAT	100
TCAACTTAA	109

40

(2) INFORMATION FOR SEQ ID :476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs

250

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :476:

10	TCTGGCGGA AGGTGGTGC GTGAAAGGTG CAGGGACAGA CTGGGTTAGA	50
15	GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA	100
20	CGGGTCACTC AGTTACGTTT AGCCACAGCC T	131

15 (2) INFORMATION FOR SEQ ID :477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :477:

30	ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTT CCTAC	50
35	ATATATGGGT AGTGAGAAC A TTATCTGTAT AACAGGAAAC TGTGATTATT	100
40	TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC	150
45	AGTGTATAA GTGAAAAGA ACTCAAAATA ACTAATACAA ATATACACTA	200
50	CGTATTAGAA TTCAAAAAG CTGCTTCTG TGAAGTCAAT CAGCTATATT	250
55	AAAAAAGACA CAAAT	265

(2) INFORMATION FOR SEQ ID :478:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 base pairs

251

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :478:

	AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATT CCAAAAGACC	50
10	TGTNTTTATT NGNNNGNGTT NGCTTCCTTT GTCATCTAGA GCCTTGTGT	100
	ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNNTT CTNTCTGTGT	150
15	NTTCATCATG GTGTTGTCTA GGTCTCCTGA GG	182

(2) INFORMATION FOR SEQ ID :479:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 169 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :479:

	AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAAACCA	50
30	CCTTCACGG TGGGGAAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA	100
	AACGGGAGCC TCTAAATCTT GGTGGGACT GCTCGCCTGG AGCCGCACTC	150
35	TTGAGTCCGA GGCCATCTT	169

(2) INFORMATION FOR SEQ ID :480:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 238 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |

252

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :480:

	AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAGT	50
	CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTCTGTC TCACCGGATA	100
10	TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATTT AACAGACCCT	150
	GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA	200
15	ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC	238

(2) INFORMATION FOR SEQ ID :481:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 201 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

	TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC	50
30	TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCCAA GTCTGCAAGC	100
	AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG	150
35	ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCTGT CTGAGGGAGG	200
	C	201

(2) INFORMATION FOR SEQ ID :482:

40

- | |
|-------------------------------|
| (i) SEQUENCE CHARACTERISTICS: |
| (A) LENGTH: 162 base pairs |

253

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :482:

10	CGGCTCAGNC TGTTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC	50
	CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA	100
	CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA	150
15	ACNTTTTTAG AT	162

(2) INFORMATION FOR SEQ ID :483:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 250 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :483:

30	ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA	50
	ATGTTAACAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA	100
	AGGCGAGGAG AGCAGGATT CTCTGCCTCT TCAAACTCNT NCCTGAACCT	150
35	GAGGGAAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA	200
	CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAAACT	250

(2) INFORMATION FOR SEQ ID :484:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs

254

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :484:

AACATTATCT TGACAAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG	50
10 AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG	100
ATTAGAATGT TAATGCCACT TTGATTAGAT CT	132

15 (2) INFORMATION FOR SEQ ID :485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :485:

TGTGGCTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC	50
20 CGCATTCACT GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC	100
30 ACGGACTTCT CGACACCATC AAGAGCGAC	129

(2) INFORMATION FOR SEQ ID :486:

- 35 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

255

(xi) SEQUENCE DESCRIPTION: SEQ ID :486:

TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG 50
5 AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG 100
ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTGT 150
10 CATTGCACCT CAACCATATC GA 172

(2) INFORMATION FOR SEQ ID :487:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :487:

ATGCTGCACA CTATGTCTCA CAAACTAAAT GGATCCATTA AAAGTTATGA 50
25 TTTAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA 100
TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC 150
AGCACTCCTC TATGGGCACA GACACACACA CAAAATTGTC CTTGCTTTTC 200
30 TCAGATATAT 210

(2) INFORMATION FOR SEQ ID :488:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC 50
5 ANACGTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT 90

(2) INFORMATION FOR SEQ ID :489:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

20 ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAAACATA CCGGGAGCCA 50
TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC 99

(2) INFORMATION FOR SEQ ID :490:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

35 GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG 50
CCCCCTCTGG ACTCCATGCA CCAAGGTCAAT GGCCAGGAGC TCTTGGCAGC 100
40 TCAGCCCTGCG CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA 150
GCTTCGGAGA TGCAGCCTCT GCAGCGAATG CCCCCGA 186

257

(2) INFORMATION FOR SEQ ID :491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- 5 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :491:

	AGCCAACTAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA	50
15	ACACTAATGC AAGAACCATC ACGGAAAACC ACCGGCAGCAG CTGAAACTTT	100
	TATAGCCCAT AAAAGGACCA ACAAGTAAG CTGAATGACT GTGAAAATAT	150
	GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG	200
20	CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC	250
	TTCATATCGG AAA	263

25 (2) INFORMATION FOR SEQ ID :492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- 30 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :492:

	AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT	50
	AAATNGGTGT GGGNGGTCCG CTTTGGCCA TCATCGCACC CCCCCGGTCA	100
40	CTGGCGTTG TTGCCGGGCA CTTGTTNNC NGGCTGGGTG TGTACCGTAA	150

258

CCGTGGGTC

159

(2) INFORMATION FOR SEQ ID :493:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15	GGGCAGAGNA AGAACTGTTC CACCAGGTGA ACAGTCCTAC CTGCTTGGTA	50
	CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT	100
	CAAATCAAGG TATCGGGAAG AATAATTCC CCTCGATTCC ACAGGAGGGA	150
20	AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT	197

(2) INFORMATION FOR SEQ ID :494:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 188 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35	GATGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA	50
	GGCGCACCA TCAGCAGCCT CACCAAGCTGT GAGCCTGCTA TCGGGCTGC	100
	CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG	150
40	GGAGGGCTGC TGTGAGTGGAA GTCTTGAGTN GGTGAGTG	188

259

(2) INFORMATION FOR SEQ ID :495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC CTTTATTGAC AATGAGAAGA TGGAGTCCCG	50
GACGCATCTA TCCCCTTTG GCCCTTACAG GTTTGCCACG AGAGTGAGAC	100
GCCTTCCTGG ACCAGGGGAG GGNGNGTTGG TNCTNTGNGC GTGNGGGTNT	150
GTGGGNGCTG CTGGGGAGG	169

20

(2) INFORMATION FOR SEQ ID :496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTTCTATGG CTGCTGCTTC TAGGAGTCTC TCGCTCATAG	50
AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TCGAAGTCCC	100
ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTGCA TTCATGATGC	150
TTTAAACCGT CAAGCTGGGT GG	172

40

(2) INFORMATION FOR SEQ ID :497:

260

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :497:

10	GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAAC CTCCCTCCAG	50
	TAAATNGGTG TGGGNNGTCC GCTTTGGCC ATCATCGCAC CCCCCCGGTC	100
15	ACTGGCGTT GTTGCCGGGC ACTTGTNNN CNGGCTGGGT GTGTACCGTA	150
	ACCGTGGGTC CTCTGACAAG TGCCCTAACTC GGCCCACCCC TTAGGGTGTG	200
	TNTCATCGAA GTGTAGNGAA TGGTGAACG TTTGTTGTN GTGTGC	246

20 (2) INFORMATION FOR SEQ ID :498:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30	(xi) SEQUENCE DESCRIPTION: SEQ ID :498:	
	GCCCCTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT	50
35	CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG	100
	CCACTATTTT TGGTGTATAT CTTCATCTCA ATGGGGACAT GGCCACTGCC	150
	CAAGGAACCTT GTGGCAGGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT	200
40	GAACATCGTG CGTTA	215

261

(2) INFORMATION FOR SEQ ID :499:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :499:

GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT	50
15 AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCCTGTTCC	100
ACANGAAAAT AAAGCTAGGG AGGTGATTAA TCTATCCGAG AAAAAAGCCG	150
20 GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT	195

20

(2) INFORMATION FOR SEQ ID :500:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :500:

GCGGCCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT	50
35 GCTCCCCACA TGGCGGGCCT TTGAGGTTCC AGTAAAATG CTTTCAACAA	100
ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTTAAA GTGCACAAAG	150
TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG	200
40 CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG	250

262

GTGGAGCTGT

260

(2) INFORMATION FOR SEQ ID :501:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15	AAAGGCATAG TAAAAATAAA ATCTACGTA GTAAACAATCT AATACTATAT	50
	TAAAATNCGTT GCTACAAAGT GTTTGTTTC TCTAAAAAGT AGTTTTGCA	100
	TATCATTCGA CCTCTTCACC CATNTGCTGG CTTATTTGCT TTATATACAA	150
20	CAGTTAAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA	200
	CAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA	250
25	ACCATGGCTT GCCCAAAT	268

(2) INFORMATION FOR SEQ ID :502:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :502:

40	AAAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG	50
	GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTCTAGAGAC	100

263

GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA 150.

CC 152

5 (2) INFORMATION FOR SEQ ID :503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

CCCTGACCCC TCCTCACCAAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC 50

TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAAC 100

20 NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T 141

(2) INFORMATION FOR SEQ ID :504:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :504:

35 CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC 50

GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG 100

40 GCCGAGC 107

(2) INFORMATION FOR SEQ ID :505:

264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :505:

10	ACCCCTCTTCT GATAAAATTTG AGGGCCCCGT TGTCCCTTGGGA GACCTTCAGT	50
15	AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT	100
	GTCCCCGACG AACTTGGTGT GTTTGGTCAG ACGCCCGCGT TNGGCNTGTG	150
	CTGGGCTTGC TCACGTTCTT GTCACTTTGT GGCCCTTGTG GAG	193

(2) INFORMATION FOR SEQ ID :506:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :506:

30	ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTTCCCTACA	50
	TATTACGGGT AGTGAGAACCA TTATCTGTAT AACAGGGAAC TGTGATTATT	100
35	TAAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT	150
	GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAAATATA ACCTATGTAT	200
	TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAACAAA	250
40	TGACACAAAT CCAAACAAGA TGCA	274

265

(2) INFORMATION FOR SEQ ID :507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :507:

	CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGTCAG CAAATTGCAA	50
15	AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA	100
	GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA	150
	AGTGGTTATC ACTAGGCTAA AACTGACAAA GACCGAAAA AAACCTTCAA	200
20	CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAAC AAGGAAGAAA	250
	CCATTGAGAA GATGCAGGAG TAAAGTATTA T	281

25 (2) INFORMATION FOR SEQ ID :508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :508:

AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG	50
CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAAACA TGAGGCATCA	100.
GCAGAGGGGA CAGAGATGAT GACCCTTCG CTCCCCCTG CAAATGAGCC	150

266

CCAGCCTTCT CCATGGTGGT GAAGACGCCA

180

(2) INFORMATION FOR SEQ ID :509:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :509:

15	AAATGCAAAA CTCACCGTGC ACACCTCTAG ATCCCTGCCA CAAAGAAATC	50
	TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT	100
	ATTT	104

20

(2) INFORMATION FOR SEQ ID :510:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :510:

35	GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG	50
	GGAAGCTAGA GCCAGAACATCA GGAAAATCTG TTTCCTCGTC CCCAGACTCC	100
	CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA	150
	GACTTGCATC TGNATCTTGN A	171

40

(2) INFORMATION FOR SEQ ID :511:

267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :511:

10

ACTGTACCTA TCATCCTGAA AAACTTTATG GGGGAGAAAG GTCAGCAGCT	50
TCTCTTTCTT TTNATCGAAA ATAATAAAC TGCGTATTCT ACTTTAACTA	100
AATGTAAGGA AGAAAATATA CAAGCCATA TTTAATGTAT TTCTATNCGA	150
GCAACAATAG TTCATATGTT CATGTTGCT ACTATCACAA TTCAACATAT	200
GAACACAGAT CAGCTCTATA CCATGAATAAC TGCTGGAAGT GATGGTTAG	250
20 GATTA	255

(2) INFORMATION FOR SEQ ID :512:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :512:

35 GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT	50
TTCTTGCTTT ATTTGTGACA TTTCAGTTA TTAGAAATCA TGTTACCATT	100
AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTTGATTT GTGTAACCTG	150
40 ATAAAAGATT TACTGACTTA AGCTTTGTT TTTTTTCATA AGCTGCTTT	200

268

GAGCTTGTC

210

(2) INFORMATION FOR SEQ ID :513:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :513:

15	CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA	50
	AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG	100
	AACAGGGATT CTTTTCTTTA CAAAAGACCC AAAGATAACGT GGACAAAAAA	150
20	AGAAAAGCTT GAAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG	200
	AAGAAACAAA CGTGTGCATC CT	222

25 (2) INFORMATION FOR SEQ ID :514:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

	GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT	50
	GAGGAGAAC GCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC	100
40	AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA	150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC 200

CTAGTCAGGA CCACAACCTCT TAAACCTCAT AGCNAAAATAT 240

5 (2) INFORMATION FOR SEQ ID :515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAAATA ATCTAANGTA 50

20 ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTTAT TCAAGACTGA 100

TCCCTATNAG GAAGGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG 150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG 183

25 (2) INFORMATION FOR SEQ ID :516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA 50

40 CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATAACACAG 100

AACACTCATA CACACANGCT TGTGCACACA TGTTCATGCA CATGCATGCA 150

270

CTCACACTCA TACAAACGCA CATTAAACA CGTGTGNACA NTGTACTCAG 200
ACACACACAG GTGTG 215

5 (2) INFORMATION FOR SEQ ID :517:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACAGA 50
GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG 100
20 TGTGCAGTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC 150
AATCATGGGC CCTAGCCGNC CTNGTAATAC G 181

25 (2) INFORMATION FOR SEQ ID :518:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

ATGTAACTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT 50
GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT 100
40 AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTG TTCATCAATA 150

271

	AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAAGTGTAT TAAAATAGAT	200
	CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA	250
5	CCTGGCAACT	260

(2) INFORMATION FOR SEQ ID :519:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 10 | (A) LENGTH: 115 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :519:

20	AAGCTAACAC AATGGTCATT TCCAGACAAA TTAAAGGAA ACACAAAGGC	50
	TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA	100
	CATGCTCTTT TTTTA	115

25 (2) INFORMATION FOR SEQ ID :520:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 30 | (A) LENGTH: 175 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :520:

	CANGTGGCTT CAATTAACCA ATNAGGAGCC TCNNAACATC CTGTCGCAGA	50
	AACTCCAAT ATAAACGCC. CCANACACTA ACACAAAACA GCCTTATTAA	100
40	CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT	150

272

GACTNATAGN TNGACCCACC TGTGA

175

(2) INFORMATION FOR SEQ ID :521:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15	ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT	50
	TCTGTGTGTG GCACTGATTG ATCAAGACAA GAGGGACATG CTTCCCTTG	100
	TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTTCA	136

20

(2) INFORMATION FOR SEQ ID :522:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :522:

35	AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG	50
	GATATATTTT GTGTCTTCTG TGACTGTTCA TTCATGGAAG GAAGCAGACT	100
	GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC	150
	TATTCCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC	200

40

(2) INFORMATION FOR SEQ ID :523:

273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :523:

10

AGTAAGGTTT TGCATCCTT GATCAGCAGG TAACTGACGA ATTCTTGAGT	50
CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA	100
CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAAACTGC	150
ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA	200
CATA	204

20

(2) INFORMATION FOR SEQ ID :524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT	50
GGCAACAAAGT GCAGGTTTT TGGCTTTCTT TGATTCAATAT TGTGCAAGAC	100
GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNNTCTAAN ATAATCCAAA	150
GAGGTCAATG TATCATCA	168

40

(2) INFORMATION FOR SEQ ID :525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :525:

10 AACTGTTCT TAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT 50
AGAACATCGA ATCACCTAAN GGAAATGGTG ACACAGGTG TCCTTCATCA 100
15 GCCGTTGGTT TCCTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC 150
ATTTAATTAA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAGTGT 200
TTATCTCCCT CTGCATTCAAG ACCAGGCTCC TTAGTGCACT CATCAGACTA 250
20 TCGCTGCCCC TGCTGTCTGC TGTTGAGCCT TCACCACCACT 291

(2) INFORMATION FOR SEQ ID :526:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :526:

35	CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAAACTCA	50
	TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC	100
	CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGCG	150
40	AGCCTGGCAT CACTGTCAAC CACCTGGCAG TTAACCGGGT ACCAAGAAGT	200

275

GGGAAGC

207

(2) INFORMATION FOR SEQ ID :527:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :527:

15	AGCATTCCGT AAGGACGGAC GTGTTCAAGG ACAACTTGATGAGATGGAC	50
	AGGTCTAGGG AGGTTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC	100
	CCAGCCAGAC TACATTTCTT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC	150
20	CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCCTGCTCC	200
	CTCTGACCCA GCTTCACC	218

25 (2) INFORMATION FOR SEQ ID :528:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

40	AACCTNATGA CTCTCCATCC CCTTGAACCA AACATCTAGC ACTCAGCTCC	50
	AGCATATTTCA ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT	100
	GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC	150

276

CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT 200

TTTACACCCA GTGTGTAAGC CAGAAGGGC 229

5 (2) INFORMATION FOR SEQ ID :529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGGCA 50

ACAAGTGCAG GTTTTGCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC 100

20 CTTAGCCTCT TTGCTTC 117

(2) INFORMATION FOR SEQ ID :530:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :530:

35 TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT 50

GAAGACCGAGA AATGATCCAG AAAGAAATGTG CTGCAATCCG GTCATTTTT 100

AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA ATTACTGTA 150

40 TATGCCACATG CTGGTGCTAC CCTCTCACT 179

(2) INFORMATION FOR SEQ ID :531:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :531:

AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAAT ATCTTCTCAG	50
15 CATTCAAAAC AAAACGCATA AGTCATTCCCT AACTTNAGAG CTTTATAGCA	100
TTTCCCTAGA CAGGAAGGGA AAAAACAGTT AGCATTAAA AGTCCGGAAA	150
20 GCTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTG TCCAAATCCC	200
TTAT	204

(2) INFORMATION FOR SEQ ID :532:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :532:

35 AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGGAGGA CGTGCCAGAC	50
CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGGAGG CGGCCTCTCC	100
40 CCACAGCTGA GGGGCTGGGC TAGGGTGGG TGGAGCCCTT TTAAATACC	150
CTTTCTCAA AACTTAGCTC TGAATGGAGA AAC	183

278

(2) INFORMATION FOR SEQ ID :533:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :533:

	GAAACAAGTT CTCGCTCATC CCTGCATTTC TGCCAACCTTC AGCTTGCAAT	50
15	ATTTATACTC CAGACTATTTC TCATCAGACA AAAACCAGTA AGCAGGGTCC	100
	TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG	150
	TTTCACAAGC TGGTTGATGG TGCCCACCTAC CCGTGATCTG CTCGCTGGGG	200
20	GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTTC CAGGTTTCGT	250
	AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT	287

25

(2) INFORMATION FOR SEQ ID :534:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :534:

	AGCCACTGCC CCTCTTGCT ACGTATTCCC AAAATTAAC TTTGATGCCT	50
	GACTTTTGCA GTCAAGTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG	100
40	GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTGT	150

279

TTAG

154

(2) INFORMATION FOR SEQ ID :535:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :535:

15	GATTACCCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG	50
	GGCCTATTTG TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA	100
	TAAAGCTACT GAAAACATATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG	150
20	GTATTTACA ACTCGCATTG CTTGAAATC TCAACACACG TAAGACTCTC	200
	CTAGGAAGGC AC	212

25 (2) INFORMATION FOR SEQ ID :536:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

	GGAAGCTCAA TGTCCGGCAG GTCAATGCTT CNCGGACACCG GATCATTTC	50
	ATCTGATTCC AGCCTGCTTG CAACCCCTGGA ATCCCTTTGT TCCCTGCTGC	100
40	CTGCCCTTG GGAAGGNACA GTGATGTCTT TAGGGGAAGG AGGAGCCCC	150

280

NTCGGCAGTT GTCTTACT

168

(2) INFORMATION FOR SEQ ID :537:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :537:

15.	CGGATCATT TTATCTGATT CCAGCCTGCT TGCAACCCCTG GAATCCTCTT	50
	GTTCCCTGCT GCCTGCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGAA	100
	GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGNNNNNTAA TGAAGTA	147

20

(2) INFORMATION FOR SEQ ID :538:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :538:

35.	GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG	50
	GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGAG AGAGATTGCT	100
	GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT	150
	GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA	200
40.	AATNAATGTA AACCCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC	250

281

(2) INFORMATION FOR SEQ ID :539:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :539:

AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT	50
15 GTGCTCTAACG GGTGCTATGT TCGATGCTGG TGTTTCGGGG ATGGTGAATG	100
CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC	150
CAGTGGGATA GGGGTGTAAA AAAGTAAATT GGGC	184

20

(2) INFORMATION FOR SEQ ID :540:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :540:

AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA	50
35 CCAGGGAAGT CACCCCACGG CTATGGAAA TTAGCCCGAG GCTTANCTT	100
CATCATCATG TCTCCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC	150
AGAT	154

40

(2) INFORMATION FOR SEQ ID :541:

282

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :541:

10

AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA 50
ATTTTGTTTT CTTCTGTGTT ATTGGTTCAA AGTACTGGCC TTTTCCTTCA 100
TTTCCAGTAA TTATTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA 150
TGATTTGGTT ATACTGTGAA ACAGC 175

20

(2) INFORMATION FOR SEQ ID :542:

25

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 221 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :542:

30

AAGTACCTTT TCCTGCAGCT GCGCGTATGC CTGAGTGACT AAGGGGCAGT	50
CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC	100
AGCCGTGCTG CTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT	150
GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAAACG CGGTCTTCTG	200
AATCGCGACT GGCNAACAGA T	221

40

(2) INFORMATION FOR SEQ ID :543:

283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :543:

10

AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG	50
GAGAAACATA CCTTGAGAGG GGGTTTCCTT TAAAACTAGT GTTAGAAGCT	100
TAGGGATTTT TTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA	150
TTTGACTTGT GCCGACATTG CAAACTTTNT GACAGG	186

(2) INFORMATION FOR SEQ ID :544:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :544:

30

AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTTCTGCCT	50
TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA	100
CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT	150
GCC	153

(2) INFORMATION FOR SEQ ID :545:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs

284

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :545:

	GATTCA	GCTC CAGCATC	CCTT GCCACCT	CCCC	GGGAG TCAAGGGTCG	50
10	TGTTCTGCC	TTGAACAGGC	CACAGCCGTA	GCTGTAGAGA	GGCCAGTGGT	100
	ACATCA	GCCC ACCGACAGGA	GGAGGAGCCC	TGGCTTGAGG	GAAGGGGAAG	150
15	CCCAGGC	CTG T				161

(2) INFORMATION FOR SEQ ID :546:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 188 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :546:

	AATAGCC	CTG AGGTCATC	CCT GC	AAAGTGCG TATCA	AAAAAA TACGAAGTTA	50
30	GGGTGAC	AAA GTTTGACAGT GATGTT	TATAC AAGTC	AAACT TGG	GAAGGTCA	100
	TAGTAAGC	CAT ACCTATG	GCTG AGAGAA	AGCA TCA	AAATC	150
35	TTTAGTTT	TA TTGTAAC	AAA GCA	ACTTG	TCA CACTTTA	188

(2) INFORMATION FOR SEQ ID :547:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

285

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :547:

	ATNCCTTCTC CATCCANTTA GTTANCAGAA ACTAATCAAA AGAAAAGTCTG	50
	ACAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA	100
10	GTATCCACAA CGTGCAGAAGG CCTACCCTTT GTGTGTACTC ATCTCACCGT	150
	TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG	200
15	AATCACTCAT TTAGAAAA	218

(2) INFORMATION FOR SEQ ID :548:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 46 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

	GGAGGGAGACC ATCAGNCCCG TGAAGACCAAC TCCTGACGTC TCGTGT	46
--	--	----

30

(2) INFORMATION FOR SEQ ID :549:

	(i) SEQUENCE CHARACTERISTICS:
35	(A) LENGTH: 146 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

286

	AGGGGGCTAA NGGTTGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG	50
	TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG	100
5	AGGGGCAAGA CACGACCTT AGTTTCCCCC TTGCGATAAN CTTCNC	146

(2) INFORMATION FOR SEQ ID :550:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :550:

	AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA	50
20	ATCCAATTAT ACTCTTCAG TTATTTAAC ATGTACAATT AAATTATTAT	100
	TGACTCTAGT CACCTGTTG TGCGAGCAAG TACTAGGTCT TATTCAATTCT	150
25	TTCTAACTAT TCCAGGCCCT TTTTAATCAA GAAGGCTCCC TAGACCAAAA	200
	TTTTAAAAAG ACAATGCTAG G	221

(2) INFORMATION FOR SEQ ID :551:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35
 40 (xi) SEQUENCE DESCRIPTION: SEC ID :551:
 AACATCGTT TATTCATCCA GCAGTGTGTC TCAGCTCCTA CCTCTGTGCC

	50
--	----

287

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG	100
--	-----

GGGAGGGGGT CATTGT	116
-------------------	-----

5 (2) INFORMATION FOR SEQ ID :552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT	50
--	----

CAGTATCGCT CCTCCCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG	100
---	-----

TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCACT	150
--	-----

(2) INFORMATION FOR SEQ ID :553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :553:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT	50
--	----

GAGGGCCTAA TCAATAAAA AAGTTAACCA TTGCGATGAC TCTACTATGG	100
---	-----

GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG	150
--	-----

NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT	189
--	-----

288

(2) INFORMATION FOR SEQ ID :554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :554:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT	50
15 GAGGGCGCTAA TCAATAAAAA AAGTTAACCA TTTGCATGAC TCTACTATGG	100
GAATAAAATTA CCTGTTTAAT ACCTCCGACTT TTTATAGAAA AATAATGATG	150
NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC	198

20

(2) INFORMATION FOR SEQ ID :555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :555:

CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCCAAC TGAAGAACTT	50
35 GAGTCTGATG TTGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG	97

(2) INFORMATION FOR SEQ ID :556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

289

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :556:

	TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAAAATTCA TCCTCTTGTT	50
10	GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA	100
	GTCTTAGGAC ACAGAGACCA GGGTGTGAA TTTTCTTCCC TGCCCCTAGG	150
15	CTGTTCAAGGT CTTCCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT	200
	CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT	250
	CTTCAAGGGT GATCTTGTT	269

20 (2) INFORMATION FOR SEQ ID :557:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :557:

	ACTCCCTCAA GGTCGTGCGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG	50
	ACCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCT	100
35	GGAGGAGAAC AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAC	150
	AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG	200
	ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCCTAGNTT NAGCC	245

40 (2) INFORMATION FOR SEQ ID :558:

290

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :558:

10	GAATTTAAAA AAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC	50
	ACAACCTTCG TTCCGCAGTT CATTAATCCG ACTCTGATGC TAAGGTGACA	100
15	GTGTATGTAA GTAGATTTT GTTTCAGTG AAGGAGACCT GGGAAAAGAT	150
	GGATTCTCT CTGTATCTTA AGAGTTATCA GAT	183

(2) INFORMATION FOR SEQ ID :559:

- | | |
|----|---|
| 20 | (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear |
| 25 | |

(xi) SEQUENCE DESCRIPTION: SEQ ID :559:

30	GTCATTTG GAAAGTGAGA TAACCAAGGA ATAATCGAA GGAGTTAGGG	50
	AGATGATTAC GTGATAATGA CTTGGGCCG TTAACCTTG ATCCCGGGTA	100
35	TGCTNAAGAA GCTGAC	116

(2) INFORMATION FOR SEQ ID :560:

- | | |
|----|---|
| 40 | (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double |
|----|---|

291

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

	CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCCTGCGC	50
10	TGGATAACGGC GACGGTTCT CATTGCCCT TGTCACTCT CATTGCGTGA	100
	GAGGCATAGA CCTTTTGAT ATCATCAGGC TTTCCGTTT TAGGAGCAAA	150
	ACAGCTTCTT	160

15 (2) INFORMATION FOR SEQ ID :561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

	GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC	50
30	AAATGCACCC CGTTCCCCTG TGGAGATCG TTTGAATNAG ACCAGAAACT	100
	G	101

(2) INFORMATION FOR SEQ ID :562:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

292

(xi) SEQUENCE DESCRIPTION: SEQ ID :562:

5 ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTGAT 50
 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100
 TATGAGGAGT GGAATTTAG ATGTCTATTA CATTNGTCTT TTAAAAGAAA 150
 AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 183

10 (2) INFORMATION FOR SEQ ID :563:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :563:

 AGAGACACGT GAAATTCTATA TCTCAAANN NC ACAGAGCTGA GACTTTGGC 50
 CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTGGTA 100
 AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150
 GATTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187

30 (2) INFORMATION FOR SEQ ID :564:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :564:

293

	GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA	50
	CACAGAAAAA TGGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT	100
5	GAGACACGAT CTAGGAAGCC TACCACTTG GCTGCTCACT GTATGCACAC	150
	AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC	200
	AANGTGACTA TTC	213

10

(2) INFORMATION FOR SEQ ID :565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :565:

	TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCGT	50
25	GGGTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCAG	100
	CCCAATACAA AATACACAGA AAAAGCAATT ATTAACATAC TGGCTTCGGT	150
	TTCTTTTTTT CCTTTAA	167

30

(2) INFORMATION FOR SEQ ID :566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :566:

294

	GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT	50
	GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT	100
5	TTGTCGATGA ATTGAGCAAC TGAGAACG	128

(2) INFORMATION FOR SEQ ID :567:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :567:

20	GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTGGA	50
	AACTAGTCCT CAATCTTCGA TTTCCCAGCA AGGACTTTCT CAGCNAGCGA	100
	TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNNTGTT	150
25	GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCCGG TTGGNNNTGGG	200
	NG	202

(2) INFORMATION FOR SEQ ID :568:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :568:

40

	ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA	50
--	--	----

295

	AAACAAATAT AGTATAAACCA TTAAACAAAT GAACAATAAT CATCAATAGA	100
	CGGGTTACTT TCAAGGAAGA GTTGTTTGT GACAAATTCT ACTCTTGATC	150
5	TA	152

(2) INFORMATION FOR SEQ ID :569:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 10 | (A) LENGTH: 181 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :569:

20	CAGGTCCGCG TGCTCTCCGC ACCACCCCAC TTCATTCCGG CCAAACCAAC	50
	CGCACCCCTG AATTTCTCCG CAAATTCCT GCCGGCAAGG TCCCAGCATT	100
	TGACGGGATG ATGGATTCTG TGTGTTGAG AGCAACGCCA TTGCCTATTA	150
25	CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T	181

(2) INFORMATION FOR SEQ ID :570:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 30 | (A) LENGTH: 157 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :570:

40	ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAAATTGCA TATCCAGTTT	50
	AACTGGACTG GGCTGTGTTG GGCGAGGATC NGCAGGGTTT TTTCCTCNNT	100

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA 150

ATGCTTT 157

5 (2) INFORMATION FOR SEQ ID :571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA 50

AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTGACC 100

20 AGGGTATGAT CTTAACCTTT TCTGAGCTGA TTTGATCGTG GTCTTACAC 150

ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTTGTTT GAC 193

25 (2) INFORMATION FOR SEQ ID :572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA 50

GAAGGATTTG AGGAGGTTGG TGGAAATTGT TGAAGGAGAG GGCGAGGAAG 100

40 AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG 150

297

CTTCCCTGTT TAAACATGA AAGTGTGGC

179

(2) INFORMATION FOR SEQ ID :573:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :573:

15	AGGACCTCTA AGACATCCTT ATGACCGACAG TTTGTCCAA GGGGATATCC	50
	ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATAACAC TTTAAAAAGA	100
	TTTTATTTCT GATTTTG CGATCTTCTT CTTGCCCATG NNGCTGTTAC	150
20	TTNGCNCGGG NAGCGGTTAA TTCTANCCGC TAGGTGTGC	189

(2) INFORMATION FOR SEQ ID :574:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :574:

35	GTGCCTCTA GGTTTGAAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG	50
	TAAAGGTGTT CATAGTTGA CTGTTCTAT GATGTTTTT CAAAGAACG	100
	TCCTTTTTG AACTATAATN CCCCNCGGTT ATTTTACCAT CACAGTTAA	150
40	ATGTATATCT TTTACGTCTC TACTCAGACC ATATTTNAAA GGGGCGCCTC	200

298

ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAAGAT CTGAATTTG 250

GTTCTAAGCA TT 262

5 (2) INFORMATION FOR SEQ ID :575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT 50

CCTGAC 56

20 (2) INFORMATION FOR SEQ ID :576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTCAA CTCCGATCTT 50

35 CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC 100

CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCCACAGCT 150

CGTATCTT 158

40 (2) INFORMATION FOR SEQ ID :577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :577:

10

GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTCTTGT CAAGGTCAGG	50
GAACAGCACC CACAGAGGGC CTCTGGTCC CTCTCTGCTC AACTCCCTCT	100
15 CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG	150
AGTCTTCCTC CTGGACTTCT GGTCCTGGTA GGCTGTGCTT CATGCTCTCC	200
TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA	250
20 CTTTG	255

(2) INFORMATION FOR SEQ ID :578:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :578:

35

GAGGAGTCCA TGCCATCCTT GATGGAAAAG AAACTGAAGA GAAAAGACAG	50
CCTGTGGAAG AAGCTCAAAG GTTCTTGAA GAAGAAGAGA GAAAATATGA	100
40 CATGATATCT TTGCTTTGA GTTCCTCACG CTCTCTGAAT TTATTAGTTG	150
GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC	200

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC 250

TCTTGAGATA GTTTTGTGTTT 270

5 (2) INFORMATION FOR SEQ ID :579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTCAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA 50

GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC 100

20 TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG 139

(2) INFORMATION FOR SEQ ID :580:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :580:

35 GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA 50

TGTCGATCC AATTATTC TTGGATAAGT TTTTCTTCC TATNCCTNTN 100

40 GTTTGATAA TATAATAAAG AAGATGAGGG GCCCA TATAGAGCTC 150
CTGAGNGAGT TTTNGGAG 168

301

(2) INFORMATION FOR SEQ ID :581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :581:

CGGAGGGCCC TGTGGGAA AAATAGGATT TTAAAAATAT GGTCATTAA	50
TTTAGGTTTT CTAACATCTA CTTGGGGATG TAGCCTCCAG TGAGGTCAGT	100
TAAGTGGGAC AGAACCGGCA GAGGGAAAGAG GTCTTGCTT CCCCTGGGCC	150
CATTCTCCCT GGCTGCCAGC CCTTGAAGTC AGAACACCAT GGGAAAATTC	200
AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA	242

20

(2) INFORMATION FOR SEQ ID :582:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :582:

GCATTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG	37
---	----

35

(2) INFORMATION FOR SEQ ID :583:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

302

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

	GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGGG	50
	ACAAGAAACA CTTACCAACA AAAATATTC AACAACCCCA AAATAACTTA	100
10	CTCACAAATA TGCAAAATT TA TCTATGGCAT AGTATTCGC ACTCGATGAC	150
	ATTTAGAGAT AAAAAATCAA ATGGAGCTT	179

15 (2) INFORMATION FOR SEQ ID :584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

	AACTGCCATG AAGTAACCTG AAGGAGGCGC TGACTGGAGG GATTGATTAC	50
	AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA	100
30	GGCGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAGCTAC ACACAATGCT	150
	TTGCGACCAC AATNCACCCT TCATTCGTA ACTGCT	186

35 (2) INFORMATION FOR SEQ ID :585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

303

(xi) SEQUENCE DESCRIPTION: SEQ ID :585:

	ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAAC TA AACTACAAAC	50
5	GCACTCACAT CGCTATAATC CTTTTAAGGA CTTAAACTTT ACTCCATTAA	100
	GACTTTTATG ACTTCTAAC A ACCTGCCAA CCTCCTCACC CCCCACTATA	150
10	CCTCGGAGAA CTTTCGCGTA ATAACCACGT	180

(2) INFORMATION FOR SEQ ID :586:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 183 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :586:

	ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTG GCTAANNNNN	50
25	NTNCTNNNTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC	100
	TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG	150
30	AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG	183

(2) INFORMATION FOR SEQ ID :587:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 35 | (A) LENGTH: 280 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :587:

304

	AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTGN	50
	ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTAACGC GCACNTTAAA	100
5	GAAGGACATC AGNGAGAACCA AGAGAGCTGT AAGACGCCTC CNTACTGCTT	150
	GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG	200
	NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT	250
10	GAGACTGATG TGACNTTCCT GGGACTGNCA	280

(2) INFORMATION FOR SEQ ID :588:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :588:

25	GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA	50
	CCCCAAGATG ATTACACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC	100
	TTTTTAACAT CATGTGCGTC TCTTGGGATC CAGCAAAAGT GTTAAGCCAC	150
30	AATGCCCTTG TGCCCTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT	200
	TNTTTGTTG CTTTTGGGG TATTTTCATT AGTATTCAG CAAATCTCAT	250
35	GATAAAGGNC AAGGNCAAGA ACTNCAGAGN ACTGACCAGA GAGGCTNGTG	300
	ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT	350
	GNGNNGCANG CTTANCTATG A	371

40

(2) INFORMATION FOR SEQ ID :589:

305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :589:

10

GAGAGAGAAC ACTCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA	50
TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT	100
GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGGCTC CCATCACAGA	150
TGCTGNTCAT TCTTNCACGG NCCCCTTTA TAAT	184

(2) INFORMATION FOR SEQ ID :590:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :590:

30

GGGGGCCCGC CGTNCACNCC CCCACACTCT TGGTAGGCAA TGCTTGTCCC	50
NATATAGTTG NNGTCTATC GAGTGACACT CTCGTTCATG GATANGGTGN	100
GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCTTN	150
AANGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG	200
CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT	243

40

(2) INFORMATION FOR SEQ ID :591:

306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :591:

10

ATTCGCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTACTGAGAC	50
NCGCATGCGC TCTCTCTACA CTAAGCTCG TCGCTNGNTN ACTTGCNGN	100
NAAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAAACTTT CAAATTCCGC	150
CCCTTTNGGC NANGCCAAC CANNCCCCC CCCTTTTNC CGNCCCANN	200
TTNGGNCTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC	247

20

(2) INFORMATION FOR SEQ ID :592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :592:

	GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAAATGC ATACTGTTG	50
35	ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT	100
	CCANGGATTA CGTTGCAATG TCTTCAAAAA TAGANAATTG ATTTTATATT	150
	TCTNGATGAA ATATAATAGT ANCTNNGCTA CTTTGGAA TGTGACAAAA	200
40	TACTATGATG ATTACAACTC ATTAAGCAT AAATNTGCAT GATTTAACTN	250

307

	CATGTTCCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA	300
	TTTANGGCNT NNGTGCTTTG TAATGATTG NCNTTAGGTG AAGGGNTACT	350
5	TTTNTNNNTNC TTCNTAGTAG ATTNGNTNN NTCTTTTAA GAGGANTCNA	400
	NTTTCATGNG TAANCATCAT CTTTT	425

(2) INFORMATION FOR SEQ ID :593:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :593:

20	CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC	50
	GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAA	100
25	CGCGTGTCAA CACATGCGCG CNNCGGCNC GCGATNCAAA GCTGAAATGT	150
	GCNNNGNCNGT CGTGNCGNA AATGTGAAAT GAACAAACAA CAATGAATGA	200
	ATGAATGTGA AAAAGAGNGN GNNTGAAAAT TNTANAGNNC CCCCCCNTNA	250
30	ANCAAAAG	258

(2) INFORMATION FOR SEQ ID :594:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

308

(xi) SEQUENCE DESCRIPTION: SEQ ID :594:

	GACCCTAACAA ATATGTACAA AAATATAAAA TGTAAATAAA AAATACAAAC	50
5	AAATTTCCTT TTTAAAGTAC TTTTAAGAAA AAAAGCAGGG CCTTGGAAAGT	100
	TTTGGTTCTT TTTTCCTCCC CTGTTGCAA TTCTCATGGT TTGGGTTGGG	150
10	TGGTGGAGAG CGCGTGTCACT CGCCGGTGC CTGCCACGT GGGCGGGCGG	200
	CTCTCTACTC GAAGG	215

(2) INFORMATION FOR SEQ ID :595:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :595:

25	GGGGCTGGTT TGGTCATCCG AGATCATTAA AAATGGCTGA CCCTAACAAAT	50
	ATGTACAAAA ATATAAAATG TAAATAAAAA ATACAAACAA ATTTCCCTTT	100
	TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTTCTTTT	150
30	TTCCCTCCCT GTTGCAAATT CTCATGGTTT GGGTTGGGTG GTGGAGAGCG	200
	CGTGTCACTCT CGGGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT	250
35	CGAAGGTGAC CACGTTTAGA TT	272

(2) INFORMATION FOR SEQ ID :596:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

309

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

	GACAAACTGT TGACACCCGG AGGCCTAACAC GAGGATTCA GCTTCCATTA	50
10	TGCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG	100
	AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT	150
	CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC	200
15	CTTCCTCAAA GAGGCTGCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG	250

(2) INFORMATION FOR SEQ ID :597:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 225 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :597:

30	CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA	50
	AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT	100
	ATCAAGAAC CAGACTGTGA TGACTGGAG AGCGGGCTGA ATGCAATGAG	150
35	TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGAACTGCAC	200
	AAACTGGCCA CTGACAAAAA TGACC	225

(2) INFORMATION FOR SEQ ID :598:

40

(i) SEQUENCE CHARACTERISTICS:

- | |
|----------------------------|
| (A) LENGTH: 210 base pairs |
|----------------------------|

310

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :598:

	ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTAGAT TTTCATTCA	50
10	AAAAAAAGTC ATTACATTT TACACTATAC ACGTTATGAT ATAATACAGG	100
	AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA	150
15	CGTGTGTTTC TGTGCTCTAA AATACCTAA GGTGGATTCA TTTAATGCAA	200
	CACCAAGGGAC	210

(2) INFORMATION FOR SEQ ID :599:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 116 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :599:

30	AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC	50
	AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT	100
35	AGAAAGTGAAG AAAA	116

(2) INFORMATION FOR SEQ ID :600:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 107 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

311

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

	ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTGTGC	50
10	CCCCGTAAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA	100
	TGGCCTC	107

(2) INFORMATION FOR SEQ ID :601:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 173 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :601:

25	ACTGCTAGTG AAATTCACAT GACTCACAAAT TCCCTTTAGC CAATGTTACC	50
	GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAAGCA CAGAGTGAGT	100
30	TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC	150
	ATTTTCTTTC CTTAGTGTAC CAA	173

(2) INFORMATION FOR SEQ ID :602:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 216 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

312

(xi) SEQUENCE DESCRIPTION: SEQ ID :602:

	GGAAGAGAAC ACATACACGA GGACCAGTAC CTGATGAGGA CAAGAGAGAT	50
5	GGGAANNNGC TGTGGAATT CTTTGGCAC CCTGGATGTT AACCCCTGCT	100
	CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA	150
10	GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCCTGGCC ATGTGGTGGC	200
	AAGTACCCAG TAGGAG	216

(2) INFORMATION FOR SEQ ID :603:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 213 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :603:

25	GAAAAAAACAA TCATGACAGC AACTCTCTA ACCACAAAAA TCACATATGT	50
	TATCTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA	100
30	TTTCTAGGGC CCTTCTTGGG GAAAGGTTCA TATAATTTAG CATACTACA	150
	TATTCAGTGA ATGCATTCA ATATTACTAT ATAACACTC TCAGCTACAA	200
	TGGTAATATA ATG	213

(2) INFORMATION FOR SEQ ID :604:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 219 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

313

(xi) SEQUENCE DESCRIPTION: SEQ ID :604:

	GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTCC	50
5	TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGACTGGACC TCTGGTCTCA	100
	ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA	150
10	CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA	200
	CTTCAAGAAG AAGAGCTGC	219

(2) INFORMATION FOR SEQ ID :605:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 104 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :605:

25	AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA	50
	CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG	100
30	NNGA	104

(2) INFORMATION FOR SEQ ID :606:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 189 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :606:

314

	AATAAAGCAT TCTCACAAACC TTTGTTGGGT CAATGATTCC TTTTTACCA	50
	ANNTACAGAA TCTCCACCAT ACCATCATA CCAAACCTCTGA GGAACCTTCGC	100
5	ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA	150
	TCGCCGGAAT TTTGAGTGT CTTTCAATAA CCTACANTA	189

(2) INFORMATION FOR SEQ ID :607:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :607:

20	GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA	50
	GAGCTCGTAT TTATCCTTG CTTTNATNTG AGACCAAGCT AGCCCTGAGT	100
25	AATTTTANNT GGTTCCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT	150
	GCCTTACGCA CATTCCCTTN T	171

(2) INFORMATION FOR SEQ ID :608:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40	GGAAAAGTNC GCATATAGCG TGCGNATAATA CTACGNCTAA GGAGAAACAA	50
----	---	----

315

	TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAACTGTG	100
	ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA	150
5	TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA	184

(2) INFORMATION FOR SEQ ID :609:

- (i) SEQUENCE CHARACTERISTICS:
- | | |
|----|----------------------------|
| 10 | (A) LENGTH: 191 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :609:

20	GGGGACAGCT NNNNNNGTTGT TTTGGAGCCT GTTGACTTTG TATTCTCTGC	50
	CTGTGATTTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN	100
	TGAGAAGGAA AACGCCAAT GCTTGGTTA TTAGAGNTTA ATAGGNAAGC	150
25	TCTGTTACAC TAGGTGTTAGA GTTCCAGAAT GTTCTTTGT T	191

(2) INFORMATION FOR SEQ ID :610:

- (i) SEQUENCE CHARACTERISTICS:
- | | |
|----|----------------------------|
| 30 | (A) LENGTH: 172 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :610:

40	GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTTGGTACAT	50
	GCATGCANTN GNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT	100

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT 150

AGGTATGATT TTATAGGNAT AA 172

5 (2) INFORMATION FOR SEQ ID :611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAAATCT 50

T 51

20 (2) INFORMATION FOR SEQ ID :612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :612:

CGCCTGAAAC TTTGAGGATA AACTTTCA AAAAAATAAA ACAGTATCTC 50

35 TTAATCACTG 60

(2) INFORMATION FOR SEQ ID :613:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

317

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT	50
CCTGGCGCA CAGCGAGACT GTCTC	75

10

(2) INFORMATION FOR SEQ ID :614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTTCGGC CGCCA	25
-----------------------------	----

25

(2) INFORMATION FOR SEQ ID :615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTACT ATGTTCCAT CTGTGAATAG CCACTGCACT CTAGCCTGGA	50
TAATATAGTG AGAACCCATC TC	72

40

(2) INFORMATION FOR SEQ ID :616:

318

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :616:

10	TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG	50
	GGAAATTTAG TGGCAGGGTC CCAGTGACCC TGTAAGAAGT GTTCTACTCA	100
15	CCAGAGTCAC TACTCCAGGT TGAGGCACATG AGGCAGG	137

(2) INFORMATION FOR SEQ ID :617:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :617:

30	GCAGGGCAGT CTTGGTGTGC AGCCCCTCTC CTCTCTGTCC CCTGACACTC	50
	CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT	100
	CAGAAATAAA GGGCCCATTT GAGGGATGAC CGCATTACAC	139

35 (2) INFORMATION FOR SEQ ID :618:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

319

(xi) SEQUENCE DESCRIPTION: SEQ ID :618:

	TCTTCTTACT ACAC TGGAAAG TCTGAAC TGG GTGCCTGTTA CCGTCGAGGG	50
5	TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG	100
	CCTNCNCTGA GNCGNGCCAG GCCATTGTTG ACACCCNNCAC CTCTCNCTG	150
10	ANNNNCCCAA CCAGCCCCAT TNCCAACA	178

(2) INFORMATION FOR SEQ ID :619:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| 15 | (A) LENGTH: 73 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :619:

	ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC	50
25	TTCTGCGGCC GCCACCGCGT GGA	73

(2) INFORMATION FOR SEQ ID :620:

- | | |
|----|-------------------------------|
| 30 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 139 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40	TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA	50
	AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTACAT	100

320

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT

139

(2) INFORMATION FOR SEQ ID :621:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :621:

15 TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAAAA CCCCACCCCT 50
 GGAAATGAGC TAAAAAAATA AACAAAATCC ACCTCCCACC TCCCTGNNCC 100
 CACTTCCTCC CATGCCCTCC AAA 123

20

(2) INFORMATION FOR SEQ ID :622:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :622:

 CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA 50
 AAAACATTTC NNGAGGAATT TTCAATTCC AGCTTAAAGA ACNNNCCAC 100
 CAACATAACC AATTTATGAA ANNNAAATTCA TTAAAAGGTAGAACCTCT 150
 TGTNNNCATG ATGGCAAGGG ACA 173

40

(2) INFORMATION FOR SEQ ID :623:

321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :623:

10

TTTATTGTAT CATGAGGCAT TGAAACATCT GAATAAAATCA ATGTCTGGGC 50

GGTGAAGGCA GCTGCTTCT CCTTCACCTTC TTTGGGTAC TAGAGCAACT 100

15

TGTCAGTAGA TT 112

(2) INFORMATION FOR SEQ ID :624:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :624:

ACTCCCTCTG CCCCCGGTCT TCTAGTGAGA GGGGGCGGAC AAGGGGGCGGC 50

30

GAAAAGAGGA GAAAGGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG 100

AGGTCTGCAT CCCCTCCCC 119

35

(2) INFORMATION FOR SEQ ID :625:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

322

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC

39

5

(2) INFORMATION FOR SEQ ID :626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA

50

20

ATAAAAATCT GAAAACATCC CC

72

(2) INFORMATION FOR SEQ ID :627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAACTACAAC CGTCTTCGAG

50

35

AAGGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT

100

CCAGATCGGT GACATCGTCA CAGTGGCGA GTGCGGCCTC TAGACAAGAC

150

40

AGT

153

(2) INFORMATION FOR SEQ ID :628:

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :628:

10

AAAAGAAGTA GGTCGTGTCG TTCTGGTTGC CCTAAGAGAA GAAGANNNCG	50
GTGCCACCT CGAGGTTAAC AGGGATATCA CTCAGCATAA TGTTAAGTGA	100
CCGGCAGC	108

15

(2) INFORMATION FOR SEQ ID :629:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :629:

30

TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA	50
CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA	95

(2) INFORMATION FOR SEQ ID :630:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

324

(xi) SEQUENCE DESCRIPTION: SEQ ID :630:

	CCAGCNCCGA AAAGCCAAGA CTTCATCAAC TACATAGGTC TTACCATTGA	50
5	CCTAAGATCA ATCTGAACTA TCTTAGCCC GTCAGGGAGC TCTGCTTCCT	100
	AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTG	139

(2) INFORMATION FOR SEQ ID :631:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20	CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC	50
	TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA	100
25	GCTGAAGTGG TGTGCTT	117

(2) INFORMATION FOR SEQ ID :632:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID :632:

40	CCAGCNCCGA AAAGCCAAGA CTTCATGAAC TACATAGGTC TTACCATTGA	50
	CCTAAGATCA ATCTGAACTA TCTTAGCCC GTCAGGGAGC TCTGCTTCCT	100

325

AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTGA GGCGGCCATT 150

GGAAGATGAA A 161

5 (2) INFORMATION FOR SEQ ID :633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

CCTGCNCCGA CGATGCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA 50

ACAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC 97

20 (2) INFORMATION FOR SEQ ID :634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :634:

CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTTGCACC 50

35 TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC 100

TTCTTCCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA 150

GAAGATATGT ATGCAACGTT CATTCAAA 178

40 (2) INFORMATION FOR SEQ ID :635:

326

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :635:

10 CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC 50
CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA 90

15 (2) INFORMATION FOR SEQ ID :636:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :636:

25 CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG 50
GATAAAATGT CATTCAAGAA TGGGGTGAGG TGGTTAGAGG GACTAGGTAC 100
30 T 101

(2) INFORMATION FOR SEQ ID :637:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

327

(xi) SEQUENCE DESCRIPTION: SEQ ID :637:

	CCGAGCACGA GACCCTGATG CACATTCTAA ATAAAAAGAA TGATGCCACAT	50
5	TTTAATAAAG CACAGCACAA	70

(2) INFORMATION FOR SEQ ID :638:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 10 | (A) LENGTH: 160 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :638:

20	CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA	50
	ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG	100
	TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC	150
25	TCGGAGCTCG	160

(2) INFORMATION FOR SEQ ID :639:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 30 | (A) LENGTH: 138 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :639:

40	CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC	50
	CGGATCACCT GTTTGAAACC ATCTCCAAG CCATGCTGAA TGCTGTGGGC	100

328

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA

138

(2) INFORMATION FOR SEQ ID :640:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15 CCGACCACCC CTTCTTTTC TTCGTCCATC CAGCACAGCA AGACCAAACGG 50
 GATTCTCTTC TGCGGCCGCC ACCGCGTGGA 80

(2) INFORMATION FOR SEQ ID :641:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :641:

30 AACTAAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA 50
 GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA 100

35 (2) INFORMATION FOR SEQ ID :642:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :642:

AGAGGACAGA AACGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA	50
5 GTTAATGTTC CATCCATGCT GCTTAAA	77

(2) INFORMATION FOR SEQ ID :643:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :643:

20 CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCCT	50
ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG	100
GGCTACAAGG ACTCGCCCTC CGTCTGG	127

25

(2) INFORMATION FOR SEQ ID :644:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :644:

GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT	50
40 GAGGAGGTTT CTCACCCAC AGATAACCCA AGACACAAAT GTGCAATTAA	100
AAGTTTATTT TAGACC	116

330

(2) INFORMATION FOR SEQ ID :645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCA	CCCCG ATT CGTG ACC AAG AAG GCT C TGT GCATT CG GGTTT CCAG	50
15	GAG ACT CAAA AGCC GAAG AA GCG AAGA AAGA GC CTAA AGG CT GCAG CAG C	100
	CAG AAAA ACA AG CAA AGG AG GA ACC CAG AC AG CCCT GCAA AG CATA CAAG	150
	AC ACT CAAG A CAG CAATT AA TCT GT CAT CA TT	182

20

(2) INFORMATION FOR SEQ ID :646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAG GCG CCGA GGTT GTAT AT TTCT AGGT GTC AGGT AT AT GA TTGC CATATA	50	
35	AT AAAA ATCT GAA AAC	66

(2) INFORMATION FOR SEQ ID :647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

331

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :647:

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTCCGA AGGATAAAAT	50
GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT	93

10

(2) INFORMATION FOR SEQ ID :648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTTG TCCCCACTGA GATGTATGAA GGTTTGGTC TCCCTGGGAG	50
TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA	100
AAAGTGCACA CCTT	114

30

(2) INFORMATION FOR SEQ ID :649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG	50
--	----

332

GGATTCTCTT CTGCGGCCGC CACCGCGTGG A

81

(2) INFORMATION FOR SEQ ID :650:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

15 AGGAGCNCCG ACAAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC 50
 AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT 100
 GTGTGACACC ACCGCATNNNT GATGACGCAT AATAAAAATA TAACTAATTT 150
20 AGACTAGAG 159

(2) INFORMATION FOR SEQ ID :651:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

35 CCGACCACCC CTTCCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
 CTCTTCTGCG GCCGCCACCG CTGGAGCT 78

(2) INFORMATION FOR SEQ ID :652:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs

333

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :652:

10	CCGACAGACG GTCATTGATT ACAACGGGGA ACCCACCGCTG GATGGTTTA	50
	AGAAATTCCCT GGAGAGCGGT GGCCAGGGATG GGGCAGGGGA TGATGACGAT	100
	CTCGAGGACC TGGAAAGAAC AGAGGAGCCA GACATGGAGG AAGACNATGA	150
15	TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG	198

(2) INFORMATION FOR SEQ ID :653:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 224 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :653:

30	CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG	50
	ATCAAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG	100
	GCATCTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA	150
35	TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAAGTTCC ATTGGTGTG	200
	TTGCTATAAT AACACTTTTC TTTT	224

(2) INFORMATION FOR SEQ ID :654:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs

334

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :654:

	CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT	50
10	GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC	100
	CCCCCAGGAG GCTCCACCCCT CAACTCAACC CAAGCAAGAG GGACAGATGA	150
15	AAAACAAAAT CCAATCAGGG CGATAAAATGG CGGGGGGTTT AATTTGGTTT	200
	CTGAGCGCAT AAAGCTAAGG AGGGGT	226

(2) INFORMATION FOR SEQ ID :655:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 167 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :655:

30	TTAAAAAAAT TCCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTCA	50
	TTTGGTAACC TGTTTAGAAT TATAAAATC ATTCATTTG GCCCAGCCCA	100
35	TACGCCAAG AGAAAACCTTC CAGACTTTTC TGATGCCATC CAGTTTGTT	150
	CTTACAAAAT GCATATT	167

(2) INFORMATION FOR SEQ ID :656:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	

335

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :656:

10	CCACCCCTTC CTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT	50
	TCTGCGGCCG CCACCGCGTG GA	72

(2) INFORMATION FOR SEQ ID :657:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 178 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :657:

25	AGAGGGTTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA	50
	TACAGAACAA AAAAACTTTC CCTTTTAAA ACTAATGTTA CAAATCTGTA	100
30	TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAAT AAGGTGTATA	150
	GTACAATGTA TTCTAAAACT GTTCCGCC	178

(2) INFORMATION FOR SEQ ID :658:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 76 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTTCCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
5 CTCTTCTGCG GCCGCCACCG CGTGGA 76

(2) INFORMATION FOR SEQ ID :659:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

20 GCCAGCGCCG AGGTTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50
AACAAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :660:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35 CCCAAACTTC TTTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT 50
TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCCATT 100
AAACACTGAT CAAACTCAGT TGTCCTTACG TTAGCATTAC TCTGTCAAG 150
40 C 151

337

(2) INFORMATION FOR SEQ ID :661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :661:

AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAACCTTCAG CCACGTCTCC	50
TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT	100
CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG	150
TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC	200
TTCACTGTGC CTGCTGAGTC AGCTTGCATC TGCCTTCG GTGCG	245

20

(2) INFORMATION FOR SEQ ID :662:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :662:

GCCAGCGCCG AGGTGCGATA TTTCTAGGCG CAGGTATATG ATTGCCATAT	50
AATAAAAACM TGAAAACACC CC	72

40

(2) INFORMATION FOR SEQ ID :663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs

338

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :663:

GCCTGCGCCG ACCATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC	50
10 AACAAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88

(2) INFORMATION FOR SEQ ID :664:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 223 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :664:

25	GCCTGCGCCG ACAAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCGA	50
	GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC	100
	CCCCACCTGC TGTTCACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG	150
30	CGCCCATAACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCGTG	200
	CGGATAGTCA CACTCCCTGC CGA	223

35 (2) INFORMATION FOR SEQ ID :665:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 70 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

339

(xi) SEQUENCE DESCRIPTION: SEQ ID :665:

5 GCCAGCGCCG AGGTTGCATA TTTCTAGGGC CAGGTATATG ATTGCCATAT 50
AATAAAAATC TGAAAACACC 70

(2) INFORMATION FOR SEQ ID :666:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :666:

20 GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAA CCAAACCAAC 100
TTTCTACGTA CCGTATAG 118

25

(2) INFORMATION FOR SEQ ID :667:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :667:

40 GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC 50
AACAAACCTAG ACGCGAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :668:

340

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10 GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTTGATCTTC AACTCTGCAT 50
ACAAGCAGA 59

15 (2) INFORMATION FOR SEQ ID :669:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :669:

30 GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50
CATGGATCCG GATCACCTGT TTGAAACCCT CTCCCAAGCC ATGCTGAATG 100
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCCAA TGGACTCGCC 200
35 CTGCTCCCAG AGCCCAC TTT 223

(2) INFORMATION FOR SEQ ID :670:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

341

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC

37

10

(2) INFORMATION FOR SEQ ID :671:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :671:
GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC

37

30

(2) INFORMATION FOR SEQ ID :672:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :672:

GCCACCGCCG ACTCCAGGCA CTCACTAAA CTCGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

40

(2) INFORMATION FOR SEQ ID :673:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs

342

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :673:

10	GCCTGCGCCG ANGCATTCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT	50
15	GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG	100
	GTGAGGGGGT TACCCCTTCC CAGTGTAAAA TATTTCCGTG GGGCTCACCC	150
15	CAAAGTATTA AAAGCAACTT TGCAATT	177

(2) INFORMATION FOR SEQ ID :674:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 77 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :674:

30	GCCTGCGCCG AGCACAAAGAC AATGACGAAC ATTTAAAAAA AAAAGAATGA	50
	CGCACATTTT AATAAAGCAC AGCACAA	77

(2) INFORMATION FOR SEQ ID :675:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 176 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

343

(xi) SEQUENCE DESCRIPTION: SEQ ID :675:

	GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG	50
5	CCGTAACTGG CGGCTATCTG TTCATAACAA ACAAACCATCA GCATATTAC	100
	ACCGCATCAC ATCGAGTGAT TATAGAAATC CATAACACACA CCGATTGCAT	150
10	AAAATCTTT TTTAGGAAAA AAACAC	176

(2) INFORMATION FOR SEQ ID :676:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 141 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :676:

	GCCAGCGCCG ACGCCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG	50
25	CCGTAACTGG CGGCTATCTG CTCATAACAA ACAAACACACA GCATATCTAT	100
	ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C	141

(2) INFORMATION FOR SEQ ID :677:

30 (i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 365 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :677:

40 CTCTAACAG ACACGAAGCT GCCCCCTCGTA CAGCCACTCG GGCGCTGACC 50

344

	ACCAAGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG ACACGTGCACG	100
	CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA	150
5	CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCAC GTGGACCTAG	200
	G TGACTGGGA GCCCACCAAG CAGGCAGTGG GCAGCGTGGG CCCCCTGGAC	250
	CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCCCAGCCCT TCCAGGAGGT	300
10	CACCAAGGAG GCCTTCGACA GATCCTTGA GGTGAGCTTG CGTGCAGATCA	350
	TCCAGGTGCT GTAGA	365

15 (2) INFORMATION FOR SEQ ID :678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

	GCCTGCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
	CAGGGAAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC	100
30	GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAAGCA GATCTTGACA	150
	GCCTTGCCCG CGAGTGCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG	200
35	TGACTGGGAG GCCACCAAGC AGGCAGTGGG GTAGCATGGG CCCCCTGGAC	250
	CTGCCGGAGA ACAATACCAAC CGCCGCCNTN GCCGCAGTCT TTCCCCGGAGG	300
	TCACCAAGGA GGCTNTTGA TAGATTTT GAGGTGAGCT TGCGTGCAGT	350
40	CATCTAGGTG CTGTAG	366

345

(2) INFORMATION FOR SEQ ID :679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :679:

	GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
15	CAGGGAAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTTGACCTAA	100
	GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC	150
	CCCCCGGGCC ACTCCCCGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT	200
20	TTATTCCCACG GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC	250
	TTG	253

25 (2) INFORMATION FOR SEQ ID :680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :680:

	GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCATA GCTCTTACAG	50
	GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGC	100
40	CCACACACCC TTCAGGAAGG GGGAGCACTG AGAACACAG CACAGGGCT	150

346

10 CAGCCTGGGA TCCCGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA 200
AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA 250
5 GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCTACGG GCTC 294

(2) INFORMATION FOR SEQ ID :681:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :681:

20 CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGCC CCGTGGGCC 50
GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG 100
CTTTTCAGT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC 150
25 TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC 200
TGCCAACCAAG AACTGACACG CGACCTCCTG GGCGCTGACG CCATTAAC 250
268
CAACGTTGGC GCCCGGCC

30

(2) INFORMATION FOR SEQ ID :682:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :682:

347

	GCCACCGCCG AGGAAAACCG TGCACGTCA GCCATGATCA ACCCCACCGT	50
	GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTG	100
5	AGCTGTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA	150
	AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTTCCCTGCT TTCACAGAAT	200
	TATTCAGGG TTTATGCGCC AGGGTGGTGA CTTCACACGC CATAATGGCA	250
10	CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC	300
	CTAAAGCATA CGGGCCCTGG CATCTGCCA ATGGCAAATG CTGATCCTGA	350
15	TACA	354

(2) INFORMATION FOR SEQ ID :683:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 148 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :683:

30	CCTCTCCGTG AGGACAGGGC AGTCTGGTG CGCAGCCCCCT CTCCTCTCTG	50
	TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCC	100
	AGTGGCGGCA GTTCAGAAAT AAAGGGCCA TTTGCGGGAT GCCGCATT	148

35 (2) INFORMATION FOR SEQ ID :684:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 307 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

348

(xi) SEQUENCE DESCRIPTION: SEQ ID :684:

	AGCACCGAGG CGCTCAAGGT CCTGGGAAC CCCAAGAGCG ACGAGACGAA	50
5	CGCGAAGGCG CTGGACTTTG AGCACTTCT GCCCATGCTG CAGACAGTGG	100
	CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG	150
10	GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGGCGCTG AAACCCGGCA	200
	TGCTCTTGCC ACACTGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC	250
	TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATT	300
15	GTGAGGC	307

(2) INFORMATION FOR SEQ ID :685:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID :685:

30	CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGAACGT ATGCTAGCAG	50
	AGCTTCTCCC CGTGAATCAC ATGCCGGAGA TCCCACCTTT AGCTGGCAA	100
	TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA	150
35	GGAGCCATCT CTAGCGGGCC CTTC	174

(2) INFORMATION FOR SEQ ID :686:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 base pairs
 - (B) TYPE: nucleic acid

349

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :686:

ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACAC ACTAATCACA	50
10 CTAGAGAAAT TCCACTGCTA CAATAAAATG TAATCGGAAG CATCTTTACT	100
TATAAA	106

15 (2) INFORMATION FOR SEQ ID :687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :687:

CAGATTTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTTCCCCA	50
30 GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAACCC AAAACCA	97

(2) INFORMATION FOR SEQ ID :688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC 50
 CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA 100
 5 CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT 150
 GAATAGAGTC TAAGCGAACG AC 172

(2) INFORMATION FOR SEQ ID :689:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :689:

20 GCCACCGCCG AGCTCACCCC TCGGGTGCAC GCCTTCCTTG GACAAGTTTT 50
 TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC 100
 25 TCGGTAGCCG TTCCCTCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC 150
 CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTTA AGCGAGTAGC 200

(2) INFORMATION FOR SEQ ID :690:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :690:

40 GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATGCGGCCCA 50

351

ACACAAATTCAAAAGTGNTCTCAAAAAACTC

81

(2) INFORMATION FOR SEQ ID :691:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15	TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA	50
	TTGAAGGAAG AACCACTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG	100
	TAACACGGAT ATGAGCTCTA GCCGCCAAG CTAGCAATGG CAACCCTTCT	150
20	GGGTCCCCCTT TCAGCATGCG GAAGCTTTTC TTCCACTMCA CTCCATAAAC	200
	AGCTGACGCT CAAAAAG	217

25 (2) INFORMATION FOR SEQ ID :692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pair
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :692:

CGGCCTTCTG GAAACCCATG AAAAAAAAAA GTTCCGCACC TCCAAGGGGA 50
GAAGAGTAAG AGACAGCTTT CA 72

(2) INFORMATION FOR SEQ ID :683:

352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :693:

10

TCTGCTGCCG	CCCGCAAGCA	GAGGGACTCG	GAGATCATGC	AGGGGAAGCA	50	
GAAAAAGGCA AACAAAGAAGA AGGAGGAACC CAAGCAGCTT TGCAGGCTTCG					100	
15	CGTCCAACCC	TCTTGCCCTT	CACCTACGCG	CCTAGAGCCA	GTCCCCACCAC	150
GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCCAGCACC GATGGCATTG					200	
20	CCTTGACCT	AAGCCTACAG	CAGGCCCTT	TTGTGCTTCC	TTCCCCTCAG	250
GCAGGCCTCTT TCCCCCTGGG CCACTCCCGG GGGTGAGGGG GTTGTCTTC					300	
CCGATGCTTT TTGTTACCGT GGGGTTGC					329	

25

(2) INFORMATION FOR SEQ ID :694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :694:

TCTGCTGCCG	CCCGCAAGCA	GAGGGACTCG	GAGATCATGG	CCTGCGCCGA	50	
ACAAATGTAC GGAATGCCGTG AGTCCCTCTG GGAGGCCA A CACGGATCCG					100	
40	GATCACCTGT	TTGAAACCAT	CTCCCAAGCC	ATGCTGAATG	CTGCGGACCA	150

353

	GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA	200
	AAATCACCAAC CAGGACACTG AAGGCCCGAA TGGACTAACCC CTGTTCCCAG	250
5	AGCCCCACTTT TTTTTTTTTT TTGGAAATAA AATAGCCTAT CTTTCG	296

(2) INFORMATION FOR SEQ ID :695:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :695:

20	GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCAACCTAA GCCCCTAAGG	50
	AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG	100
	CGTGTCTTAG CACTAACCTC CTCCCTAGCC CCTTATTGG TGGCAGAAGT	150
25	GGCCTCCACC CCTTCACCGT TAAAAAATAC TCCGTGGAGA AAAGAAAGCT	200
	TNAAGGAGTA G	211

(2) INFORMATION FOR SEQ ID :696:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40	(xi) SEQUENCE DESCRIPTION: SEQ ID :696: GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC	50
----	---	----

354

CCAACAAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG

92

(2) INFORMATION FOR SEQ ID :697:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs.
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :697:

15	GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC	50
	CTACCAAGCAA GGGGTCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG	100
	GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCCTGCG GCTGATGGCC	150
20	ATAGTCAAGA GAAAGGATTCTGAAAGGCAG CCCTAGAAGC GGAGTTAGGA	200
	GCTTCTAACCCGTCATGGTT TAAATACACA CCCTTTTTG GACAGCGCTT	250
25	CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCTATGCG	300
	GCATGCGTAC CTGT	314

(2) INFORMATION FOR SEQ ID :698:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :698:

40	GCCACCGCCG AGTTCACCCCC TGCAAGTGCAC GCCTCCCTGG ACAAGTTCCT	50
----	--	----

355

	GGCTTCTGTG ACCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT	100
	CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCCTCCCCT	150
5	CCTTGCACCG GCCCTTCCTG GTCTTGAAAT AAAGTCTAAG CGGGCAGC	198

(2) INFORMATION FOR SEQ ID :699:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :699:

20	GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG	50
	CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAAGTGA ACAGAACATGAC	100
25	CTTCCTACGC ACAACACAAA CACCAAGTTAA TGCTCCATCC ACGCTGCTTA	150
	AAGAGCATTC CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCCACCC	200
	TTAGCCGGCA TGCTTACATT AATAGCTAGA	230

(2) INFORMATION FOR SEQ ID :700:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :700:

40	AGCAACAAAA ATGTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT	50
----	---	----

356

	GGAGGCCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC	100
	AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCT	150
5	GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCCACCCCTC ACTTGGCATG	200
	CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA	250
	GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC	282

10

(2) INFORMATION FOR SEQ ID :701:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :701:

	GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCTCT GGGAGCCAA	50
25	CATGGATCCG AATCACCTGT TTGAAACCCT CTCCAAGCC ATGCTGAATG	100
	CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC	150
	GAGAAGGACA AAATCACCAAC CAGGACACTG AAGGCCCGAA TGGACTAAC	200
30	CTGTTCCCAG AGCCCACTTT TCCCTATTT TGGAAATAAA ATAGCCTGTC	250
	TTTCG	255

35

(2) INFORMATION FOR SEQ ID :702:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

357

(xi) SEQUENCE DESCRIPTION: SEQ ID :702:

5 GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAAA AAAAGAATGA 50
CGCACATTTT AATAAAGCAC AGCACAAACT GTTCTTTCC 89

(2) INFORMATION FOR SEQ ID :703:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :703:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCCTCA 50
CGGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG 96

(2) INFORMATION FOR SEQ ID :704:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :704:

35 GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCA 50
ACACGGATCC GAATCACCTG GCGCGAAACC ACCTACCTAG CCATGATGAA 100
40 TGCTGAGGAC CCAGATGCAG TAC 123

(2) INFORMATION FOR SEQ ID :705:

358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :705:

10	GCTTGATGCC TGCGCCGAAC AAACATACAG AATGCGGCAG GTCCCTCTGG	50
	ACGCCAACAA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT	100
15	GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCC	150
	ACATCACCGA GAAGGACAAA ATCACCAACCA GGACACTGAA GGCCCCGAAATG	200
	GACTAACCT GTTCCCAGAG CCCACTTTTT TTCTTTTCA GAAATAAAAC	250
20	AGCCTGTCTT TC	262

(2) INFORMATION FOR SEQ ID :706:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :706:

35	GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACTGAG GCCCCTGAGG	50
	AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG	100
	CGTGTCTTAG CACTGCCCTT CCTCCCTAGCC CCTTATTGG CGGCGGAAGC	150
40	GGCCTCCACC CCTTCCCTGT TTGCAAACAC TCTGCGGAGA AAAGAGGACT	200

359

TCAGGGACT

209

(2) INFORMATION FOR SEQ ID :707:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15	GCCACCAACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC	50
	TCGGAGATCA CGCAGCAGAA GCAGAAAAAG GCAAACAAGA AGAACGGAGGA	100
20	ACCCAAGCAG CTTTGCAGCT TCACGCCAA CCCTCTCGCC CTTCACCTGT	150
	GAGCCTGGAG CCAGTCCCAC	170

(2) INFORMATION FOR SEQ ID :708:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35	GCCACCGTCG AGGATTCAAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCG	50
	ACGTTCCGTT TCCCCCTGCC CGCCTTTTC CGCCACCACC GCEGCCGCCT	100
40	TCTGCAGGCC GTTTCCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA	150
	CCCAGAACCT	160

360

(2) INFORMATION FOR SEQ ID :709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AACTAAACT GCAAACTCCT

50

15

G

51

(2) INFORMATION FOR SEQ ID :710:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA

50

30

CAGGATTCTC TTCT

64

(2) INFORMATION FOR SEQ ID :711:

35

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

	CCAGCCAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT	50
5	CTCTCTTGGG TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC	100
	TGGG	104

(2) INFORMATION FOR SEQ ID :712:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :712:

20	CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT	50
	TTGTTTTAG TTGAAGGC	68

(2) INFORMATION FOR SEQ ID :713:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :713:

	AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT	50
	GCTGGGCATG ATCTTCAGCA TGTGGGGCCT CATGCTTAAG CTGAAGTGGT	100
40	GTGCTTGGGT CGCTGTCTAC TGCTCCT	127

362

(2) INFORMATION FOR SEQ ID :714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC

50

15

CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATT

90

(2) INFORMATION FOR SEQ ID :715:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA

50

30

ACAAAAATCT GAAAACATC

69

(2) INFORMATION FOR SEQ ID :716:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

	GCCGAGGAGA ACCCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAAA	50
5	CCACCAACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT	100
	AA	102

(2) INFORMATION FOR SEQ ID :717:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

20	AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT	50
	GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT	100
25	GTGCTTGGGA TACGCTGTCT ACAG	124

(2) INFORMATION FOR SEQ ID :718:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :718:

40	GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA	50
	TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCCTTGAG CTGTTGCAG	100

364

ACAAGGTCCC AAAGACAGCA GAA

123

(2) INFORMATION FOR SEQ ID :719:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15	ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC	50
	TTCT	54

(2) INFORMATION FOR SEQ ID :720:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :720:

30	GACCACAGGG CCTTCAATCC TTTTTGTTT TCAACAGTCT TGCTGAATTA	50
	AGCAGAAAGG GCCTTGAAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT	100
35	AATAAAACTG TGCACTC	117

(2) INFORMATION FOR SEQ ID :721:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

365

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT 50

CTTCT 55

10

(2) INFORMATION FOR SEQ ID :722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC 50

25

ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT 92

(2) INFORMATION FOR SEQ ID :723:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAAA TCTGAAAACA 50

40

TCCCC 55

366

(2) INFORMATION FOR SEQ ID :724:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :724:

	GTGTACTATT AGCCATGGTC AACCCCACCG TGGTCTTCGA CATTGCCGTC	50
15	GACGGGCGAG CCCTTGCGGC GCGTCCTTG AGCTGTTGC AGACAAGGTC	100
	CCAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
	TTTGGTTATA AGGG	164

20

(2) INFORMATION FOR SEQ ID :725:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :725:

	GTGAGAACGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC	50
35	ACACCCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC	100
	AAGTTCAGTA	110

40

(2) INFORMATION FOR SEQ ID :726:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs

367

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :726:

	CCGTGTACTA TTAGCCATGG TCAACCCAC CGTGTCTTC GACATTGCCG	50
10	TCGACGGGAG CCCTTGGCGC GCGTCTCCCT TGAGCTGTTT GCAGACAAGG	100
	TCCCCAAAGAC AGCAGAAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
15	TTTGGTTATA AGG	163

(2) INFORMATION FOR SEQ ID :727:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 105 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :727:

	GAGGGCGAGT TCGAGGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA	50
30	GTCACTGGGG AAAGCAGGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC	100
	CTGTT	105

35 (2) INFORMATION FOR SEQ ID :728:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 186 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :728:

	GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG	50
5	ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCC	100
	AGGAAGGCAT CTTTGCAG TGGATTGCC TCAAGGTCGA GGCGCCACT	150
10	GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA	186

(2) INFORMATION FOR SEQ ID :729:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 167 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :729:	
	GCCAGCGCCG AGGTTGCATA TTCTAGGCAG AGGTATATGA TTGCCATATA	50
25	ATAAAAAACCT GAAAACATCC CACCCGGAA AAAAAAAAAA AAAAAAAAAA	100
	AAAAACACCC CCCCCCCCACA AAAAACTCAA ATTCCCCCTCC CAAAAAAACCC	150
30	CCTCAAAATC AAAAAAAC	167

(2) INFORMATION FOR SEQ ID :730:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| 35 | (A) LENGTH: 64 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :730:	

369

GCCTGCGCCG ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA	50
CAGGATTCTC TTCT	64

5 (2) INFORMATION FOR SEQ ID :731:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

GCCAGCGCCG AGACCCCTGGC GGCCCTACCGG CCCCCCGTGC ACCCCCGCTA	50
GCGCCCCACC CGCGGTCTAT CGCCAATAA AGGCATCTTT GCCGGG	96

20 (2) INFORMATION FOR SEQ ID :732:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - 25 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :732:

GCCTGCGCCG ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA	50
CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA	84

(2) INFORMATION FOR SEQ ID :733:

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

370

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

GCCAGCGCCG AGATCCTGGC GGCTTACCGG CCCTCAGTGC ACCCCCCTA

50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG

96

10

(2) INFORMATION FOR SEQ ID :734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :734:

GCCAGCGCCG AGATCCTGGC GGCTTACCGAG CCCTCCGTGC ACCCCCCTA

50

25

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG

96

(2) INFORMATION FOR SEQ ID :735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :735:

GCCAGCGCCG AGATCCTGGC GGCTTACCGAG CTCTCAGTG CACCCCACT

50

40

AGCACCCCCAC CCCGCATCTA TCGCCCAATA AAGGCATCTTT TGCCGGG

97

371

(2) INFORMATION FOR SEQ ID :736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :736:

GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTGTTTT CAACAGTCTT

50

15

GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA

100

TACAGCATTA ACAAAACCGC GCATCTC

127

(2) INFORMATION FOR SEQ ID :737:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :737:

50

GCCTGCGCCG ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA

CAGGATTCTC TTCT

64

35

(2) INFORMATION FOR SEQ ID :738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

372

(xi) SEQUENCE DESCRIPTION: SEQ ID :738:

5	GCCAGCGCCG ACAATGCCCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC	50
	AACAAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88

(2) INFORMATION FOR SEQ ID :739:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :739:

20	GCCAGCGCCG AGATCCTGGC GGCTTACCGC CCCCCGTGCA CCCCCGCTAG	50
	CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTG CCGGG	95

(2) INFORMATION FOR SEQ ID :740:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :740:

35	GCCACCCCGA AGACGTATCA AGCCCCTCGA ACAACCCCGA GAGCTGATGA	50
	GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCC CTGCTGCAGA	100
40	CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTCCAAGGA	150
	CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT	200

373

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA

245

(2) INFORMATION FOR SEQ ID :741:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :741:

15 GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTCGTCTAT CACTCTCCCC
 AACAAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG

50

88

(2) INFORMATION FOR SEQ ID :742:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :742:

30 CCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAAATATTC
 GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA

50

100

35 CTCTGATAGT CTTCATTCTGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG

150

AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT

200

CGAGTCATGT CATATACTT GCTGGATTAA TGGATGTCAT TA

242

40

(2) INFORMATION FOR SEQ ID :743:

374

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10

GCCTGCGCCG ACCACCCCTT CCTTTCTTG ATCTAGCACA GCAAGACCAA

50

CGGGATTCTC TTCT

64

15

(2) INFORMATION FOR SEQ ID :744:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :744:

30

GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT

50

AATAAAAATT TGAAACAT

69

(2) INFORMATION FOR SEQ ID :745:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :745:

375

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT	50
AATAAAAATC TGAAAACATC CCAC	74

5 (2) INFORMATION FOR SEQ ID :746:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACCATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC	50
AACAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG	88

20 (2) INFORMATION FOR SEQ ID :747:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - 25 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC	50
AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG	88

35 (2) INFORMATION FOR SEQ ID :748:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - 40 (C) STRANDEDNESS: double

376

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :748:

GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTTT	50
10 GCGCTTCCTT CCCCTCAGGC AGCCTTTTC CCCCTGGGCC ACTCCCCGGG	100
15 GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATTCCCGTG GGGCTCACCC	150
CAAAGCATTAAAGCAGCTT TGCAATTC	178

15 (2) INFORMATION FOR SEQ ID :749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :749:

GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG	50
ACCTAACGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCCT	100
30 AGAAAGGCAT CTTTCGCCAG TGGATTGCC CCAAGGTTGA GGCGGCCATT	150
GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCCAT	200
35 TGGCGCTGCT GCCTATAACA AACACTTTT TTTTT	235

(2) INFORMATION FOR SEQ ID :750:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

377

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTC ATCCAGAAAA GCAAGAGAAA 50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT 87

10

(2) INFORMATION FOR SEQ ID :751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCTGTGACC AAGAAGGCTC TATGCATTCA GGCTTCCAG 50

25 GAGACTCAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC 100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC 150

30 ATGCCAAAGA CACTCAAAGA 170

(2) INFORMATION FOR SEQ ID :752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

378

GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT	50
AATAAAAAAA TGAAAACACC CC	72

5 (2) INFORMATION FOR SEQ ID :753:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

GCCAGGCCGG AGGACACCAA GAAGGTTTG GACAGCGTGG GCATCGAGGC	50
GGACAACAAC CAGCTAACCA AGGCCATTAG TGAGCTGAAT GAAAAAAACA	100
20 TTGAAGACGT TATTGNCCAG GA	122

(2) INFORMATION FOR SEQ ID :754:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :754:

35 GCCACCGCCG ACTGAAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA	50
GGTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCCTC	100
40 AGGCGCCACC TTCACCTGGA CACCCCTCAAG CGGGAAAGAGC ACTGTTCAAG	150
GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG	200

379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT

243

(2) INFORMATION FOR SEQ ID :755:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :755:

15	GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT	50
	AACAAAAAACC TGAAAGCATC A	71

(2) INFORMATION FOR SEQ ID :756:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :756:

30	GCCACCGCCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG	50
	GGCGCGCGGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT	100
35	TAGTGCTTTT TCAGTGGGGC GGGGCGGGAA GCAGGGCGGGA CCAGGCAGCC	150
	AGTTCTAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA	200
	GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCC TGA	243

40

(2) INFORMATION FOR SEQ ID :757:

380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :757:

10

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA

50

CAGGATTCTC TTCC

64

15

(2) INFORMATION FOR SEQ ID :758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

30

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGGGGGA CCAGGCAGCC

150

AGTTCTAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

35

GACGTCGACA ACCAGAACTG ACGTGCGACC TCCCGGGCGC CGA

243

(2) INFORMATION FOR SEQ ID :759:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

381

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :759:

	GCCACACCAAG ACTTTCGACC CCCCAACCCCT CTGAGGAAGA TGGGGGCAAG	50
10	AAGATCACGC TCCCCGCCGT TTCCCCCGCC GCTTTCTCC TCTCTTCTCT	100
	CTTCGCTCTC AGCTCCCCCT GTCCCCTCAG CTCCAGACGT AGGGGAGGGG	150
	TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA	200
15	TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTC GGCCA	245

(2) INFORMATION FOR SEQ ID :760:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 68 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

	GCCACCGCCG AGGT CGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT	50
30	AACAAAAAACC NTGAAAAC	68

(2) INFORMATION FOR SEQ ID :761:

	(i) SEQUENCE CHARACTERISTICS:
35	(A) LENGTH: 71 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

382

(xi) SEQUENCE DESCRIPTION: SEQ ID :761:

	GCCAGCGCCG AGGTTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT	50
5	AATAAAAAACT GAAAACACCC C	71

(2) INFORMATION FOR SEQ ID :762:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| 10 | (A) LENGTH: 88 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :762:

	GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC	50
20	AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88

(2) INFORMATION FOR SEQ ID :763:

- | | |
|----|-------------------------------|
| 25 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 223 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :763:

35	GCCTGCGCCG ACAAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCGA	50
	GAAGTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC	100
	CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG	150
40	CGCCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG	200

383

CGGATAGTCA CACTCCCTGC CGA

223

(2) INFORMATION FOR SEQ ID :764:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :764:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
 AATAAAAATC TGAAACACCC 70

(2) INFORMATION FOR SEQ ID :765:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :765:

30 GCCAGCGCCG ACCGGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
 TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAA CCAAACCCACC 100
 TTTCTACGTA CCGTATAG 118

35

(2) INFORMATION FOR SEQ ID :766:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

384

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCTAT CACTCTCCCC

50

AACAAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG

88

10

(2) INFORMATION FOR SEQ ID :767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTC AACTCTGCAT

50

25

ACAAGCAGAA GCAATAAACCC AATCTGATTT TCTTTTCAAT T

91

(2) INFORMATION FOR SEQ ID :768:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAAGCCAA

50

40

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG

100

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150
GAGAAGGACA AAATCACAC CAGGACACTG AAGGCCGAA TGGACTCGCC 200
5 CTGCTCCCAG AGCCCCACTTT TTT 223

(2) INFORMATION FOR SEQ ID :769:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :769:

20 GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC 37
25

(2) INFORMATION FOR SEQ ID :770:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC 37

35 (2) INFORMATION FOR SEQ ID :771:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

386

(xi) SEQUENCE DESCRIPTION: SEQ ID :771:

5 GCCACCGCCG ACTCCAGGCA CTCACTAAA CTCGATCTC AACTCTGCAT 50
ACAAGCAGAA GCAATAAACCC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :772:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :772:

20 GCCTGCGCCG ANGCATTCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT 50
GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCCGGG 100
GTGAGGGGGT TACCCCTTCC CAGTGTAAAA TATTTCCGTG GGGCTCACCC 150
25 CAAAGTATTA AAAGCAACTT TGCAATT 177

25

(2) INFORMATION FOR SEQ ID :773:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :773:

40 AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCCA 50

387

	GAATTAGAGG TAAAGGAATC CTAATAAAA GAGCACAGCA GCAATCACAC	100
	TCACAGGGTC CAGAGGCGTA TTCCCTGGCCA TCTTCCTAGT ACTCGGTCCG	150
5	T	151

(2) INFORMATION FOR SEQ ID :774:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :774:

	ATCTTAATGA ACATGGCATT TAAAATCCTG TAATTTCAAA CAGTGAACCA	50
20	CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA	100
	CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC	150
25	ACTATGGAGC ACACAACCTCT GCCTCGCGCT GACACCAGAC AAACACGGCG	200
	GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG	250
	AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA	299

30

(2) INFORMATION FOR SEQ ID :775:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :775:

388

TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTGCCATTG	50
TGGCGTAATT TTCTGTGCCGA GTGAATGTGG CGCAAACAAAC TATATATCNA	100
5 AACCGTATAT TTAAAATGAA TTACTAGAGA GGGAAATGTAA TCATGGCAAA	150
AGAAATTAAG TTTTAAGAAG ATGCTAGTGC TAAGC	185

(2) INFORMATION FOR SEQ ID :776:

10

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :776:

20

ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCGCCA	50
TTTCACCACA CATGGCAACA AACTTACCTT CTTAAGAGC GGCAGTAATC	100
25 ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA	150
AGCAACCTTA TCATTACAC GATCTGCAGC CATCGTATAA CCAATCAAAT	200
CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAA CTCATCAGCC	250
30 AACAT	255

(2) INFORMATION FOR SEQ ID :777:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

389

(xi) SEQUENCE DESCRIPTION: SEQ ID :777:

	AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA	50
5	AGGCCGTACAT AAAGTAACCTT GAAAATTCG TTCTTGGCTG AATCGTGTAA	100
	AACCGTTGTA CACAACGTAG TAAAATTCAACACCATCTG CATAACCAATC	150
	GTCAGCCGTG ATGCATTTAC TCACCTTACG TCGATGAATG TCAAACATCG	200
10	CACCTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT	239

(2) INFORMATION FOR SEQ ID :778:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :778:

25	ACTGAACAAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA	50
	AATAAAAGTTG GTATTGTTTG AAGCAGCCCCA ACAATTTCGA ACATGCTACA	100
	AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAAACG	150
30	TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG	200
	ATTTTTAAGG ATGACTCAAC TTGGCCAAT CGGTTCCCTCA TTAGGACAAC	250
35	TA	252

(2) INFORMATION FOR SEQ ID :779:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

390

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

	TCGGATTTAT ACGGCTGTTA GTGCTATCGG CGTCTGGTAT GTGTTATATA	50
10	TCGCCTATCG TTTTTGGCC AATGGGCCTT GGCTACGCGG GGCAATGATT	100
	GCCATCGTTT TTGTTATCTT GACTTATTC GTCATTTAA ATATTATTTA	150
	ACTATTTAC AAATAAAAGTG GTCAAATGGG ATATTTGCC AAAAATAGAG	200
15	AAAGTGTAG GCGGCCACA GCTGGAGGAA GAGAAAGCGG CTGTGCATGA	250
	AGTTATTGCA CCCGC	265

20 (2) INFORMATION FOR SEQ ID :780:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :780:

30	CTCAGCTGGA CCAAATTAGT TGAATTACTC ACCATCAATA AACTATAAAT	50
	GGCGCCAATG ACCAACCCGC CAACGATTCC CGTTGTCAA GAACCTAATA	100
35	ACAAGTAACC AACCGCAGCC CCAACAAGCC CAACTAGGTT TAAAAAAACC	150
	AAGCAAAAGG CCAACTGTCC GTCGTTTATT GGATTGTATC TGCTCATATA	200
	ACATTAAAAAC TTAACCGTTG GCACCTCTTT CTCAGACCCG CCGATACTG	249

40 (2) INFORMATION FOR SEQ ID :781:

391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :781:

10

GAGAGAAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG	50
CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT CGGGAGGCC	100
TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNACTA CTTCCCGCAC	150
TTCCGACCTGA GCCACGGCTC TGCCCAGGTT AAGGGCCA	188

(2) INFORMATION FOR SEQ ID :782:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :782:

30

AATATTTATT TCATTTGTTT ACTACCACTT CATTATTTATTT GTTTGCTGCT	50
GCCGTTTTAT TTATTTTAC TGAAAGTGAG AGGGAACCTTT TGTGGCTCC	100
AACCTTTTTC TGTAGGCCGC CTAAAGCTTT CTAATTTGG AACATCTAAC	150
AAGCTGAAGN GGAAAAGGGG GTTTCGCAAA AT	182

(2) INFORMATION FOR SEQ ID :783:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

392

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :783:

	CACAGCCAGA GCTTCGTCTT CAGTGACCAAC AGGGCTGAGC CAGGCTCAAC	50
10	CGGCCTTCTGG CTCTTGTTT GCAGAAAGAAG AACTAGAAGC AAGGNGCTTT	100
	CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT	150
15	TTCCTGAGTT CCTGACCCCT GCTATTAT TAGTCAGCTC TCAGCACTTA	200
	CCAGAGGAAC AGGCAGCCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG	250
	AGAGAATTCA AATGCGTGT GGTGTTCTG TTAGTACAAG CAGCA	295
20		

(2) INFORMATION FOR SEQ ID :784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :784:

	CAATAGCGAC TTCTGGTGTCA ATTCTGATAA TCGGCCAATG GATACTTCAC	50
35	GTGTGTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCACT TCAGAACCG	100
	TACCTGATGT TGTTGGAATG GCAACCATT GTGTCAAACCG CACTGGTAGA	150
	ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTGTTC TATTTCCATG	200
40	AACAAATTCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT	250

393

TGAGTATTG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC

295

(2) INFORMATION FOR SEQ ID : 785:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 785:

15	GTGTAAAGCG AGTAGCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA	50
	CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTTGGTTTC	100
	ATTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC	150
20	CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAA	200
	GCGCTTTGAA TACTGTTCTG GGTTCACGGT GGAGATCTCC GCGCAGCCAT	250
25	GTAAACAGT TTTTGCAGCA TGGGCAGCTT TCTTTTTGCA ATCATAATGA	300
	GTA	303

(2) INFORMATION FOR SEQ ID : 786:

- 30
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID : 786:

40	TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT	50
----	--	----

394

CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTGACG ACTGCTTCAT 100
ACATGAAGAA TGATGGTGT CGTGGGCCA TTAAGTACTA AGCCAAGAAG 150
5 TTATCACGAC AACCTATAAC TTGGGCCAA TTAACTTGAT GATGCACGGG 200
GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA 250
CTGGC 255

10

(2) INFORMATION FOR SEQ ID :787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :787:

CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTTAAATGTG TGTGAGATTG 50
25 TCAGAACCAA CAAAACCTAGG TTGGTTAAC ATATCTCTGG TACATCAAGG 100
GGCATGATAC AAACCAGTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG 150
ACTTATTTTT ATTTTTTTT TTTTGGACAG ACTCCCTTG TCCCCAGGCC 200
30 GGAGTG 206

30

(2) INFORMATION FOR SEQ ID :788:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

395

(xi) SEQUENCE DESCRIPTION: SEQ ID :788:

	ACAAATAGCG ACCTCCTGGA GAAAATCGA AAACGGCCAA GTGGATAACCT	50
5	CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCGAG	100
	TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTTCAAAC GAGGCCTGGA	150
10	AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG	200
	GAACAATTCC GCGACACCCCT TCGTCTGACA AAAAACCTTC GTGACCGCTC	250
	GAGTATCCGC	260

15 (2) INFORMATION FOR SEQ ID :789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

	AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC	50
	TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT	100
30	GGAGAGGATG TTCCCTGTCT TCCCCACAC CAAGCCCTAC TTCCCGCACT	150
	TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG	200
35	ATCGACGC	208

(2) INFORMATION FOR SEQ ID :790:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

396

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :790:

	AAAAAGAAGTA CGGTAAGGCA AATCCTGAAA TTAAGAGTTA CTATGTGCCT	50
	GAAAATACAT TGTTCTACTC ATTTAGTGTG ATGGCAATGG GCGCCGGCGC	100
10	ACTCTTGCTA TCGACCACCG TCGCGCTTTG GATGAACCGT CGTAAGTCAC	150
	AATTAATGTA GACACAACGT CGATTCTCGT GACTTATGGG GATCGCAACT	200
15	TTCGCGCCAT TCTCGATCAA CACAGCCGGT TGGTCAGTGA CTGAATTAGG	250
	TCGTTATCCA TGGGTTGTTT ATGGCTTGAT GCTAATAGC	289

(2) INFORMATION FOR SEQ ID :791:

- | | |
|----|-------------------------------|
| 20 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 232 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 25 | (D) TOPOLOGY: linear |

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :791:

30	TTTCCTGTGG AAGTAGTTAA ATTGATAAAT TCCAAAATT TGGCAATTAA	50
	TTGCTCATTA TTAATGGTAG AGTTCCATT AATGAAGTTG GAAAATACGG	100
35	TGAATCTTTC AATGAACTCA GTTAGACATT CGGAATGAGC TTCATACATT	150
	GTCTTATTAT CTTTCTTCAA TTTATCCTCC AAATCTGGGA ATTCTGATAA	200
	CCAAATTGAA GCACCTTATC TATGATCCGG GC	232

40 (2) INFORMATION FOR SEQ ID :792:

397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :792:

10

TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC	50
TGGTAATATC GAACAAACTA TTTTAAGAA CTTGATTCT GGCAACATTA	100
15 AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG	150
GCGATCGCAT TAGATTCAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA	200
TGCCTATTTC GCGAACTATG GATCTAAATA AC	232

20

(2) INFORMATION FOR SEQ ID :793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTCACCGTA CTGANCCAG TGACCAGATG TCTTATACAA	50
35 GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA	100
ATTCTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCC	150
ATTGGTAAC CAAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA	200
40 ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTACGTTC TTTAGCTTCT	250

398

TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT

292

(2) INFORMATION FOR SEQ ID :794:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :794:

15	CAGCAGGCAC AACACCATCG GTTGTGCGTG AAAGTATTAA TAAAGTCTTG	50
	GCCAAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACATTATG CGGGTATGCA	100
	TGATGTCATT CCTGCATCCG ATGATTTTA ATTAATTACA ACAACTGATG	150
20	ATGAAGCGTC GAATTGCGTG CGTCATTCTG CCTCACACTC ACAGGCACAA	200
	GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC	250
25	CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC	288

(2) INFORMATION FOR SEQ ID :795:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :795:

40	GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT	50
	CGATAGACCC AAAAAGTGTT TTAACCTGGAA AACACCTTAT GAGGTTTATT	100

399

TTGATGAAGT GTTGCAGTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT	150
CTCAATCACC GCATTTCCA CAACCGCCA CAAAACAGCT CGTCTATTTC	200
5 GAGGTCAGTT ACGGCGTCCA GTCTTGAGC AGATGATTG CCCCGAGTGA	250
TCGTCGGC	258

(2) INFORMATION FOR SEQ ID : 796:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID : 796:

20

TGCTTCAAAG CCTGGCTTAA CCCGCTTGCC CACCAAATTC AATTATAACCT	50
GCCCCTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC	100
25 CGCGACTCGA TCCCCATCGT AAAATGATTG CGAACTAACCA TTTAACACAC	150
AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG	200
AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAAGGAC TAGCGGTACG	250
30 CTCATGTAAC GCGACAATAT	270

(2) INFORMATION FOR SEQ ID : 797:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

400

(xi) SEQUENCE DESCRIPTION: SEQ ID :797:

	AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC	50
5	TTGTGTAGGT TGTCTGAAAC GGTCCGAGTC ACCGGTTAGC TTGATAAGTC	100
	AGGTTTCAG CAACTGTCA T CAAGCCATCA CGACCTATAT AAGCCACTGC	150
	AATCGCACTT TACATCATTA AGACCCTTAC TAGAAGTAAC TGGCCATCCT	200
10	GCCACCGCTT	210

(2) INFORMATION FOR SEQ ID :798:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :798:

25	ATCATAAGCG CTGGAACCTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT	50
	GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGGCGCTCC ATAGGAAAAAA	100
	CCACGGTCCA AGGCAAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA	150
30	TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCAAA TAACGAGACA	200
	AGTAGTTGAG CTAAATGC	218

35 (2) INFORMATION FOR SEQ ID :799:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 176 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :799:

	CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCAGA CGTAGAGCTG	50
5	AGAATAGCAT TACCAAATGG AACAAACGTGC TACAGTCAGG ATTAAAAAGA	100
	ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG	150
10	AACAATACAA CACTGAATT A CTCGGC	176

(2) INFORMATION FOR SEQ ID :800:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 254 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :800:

	GCAATTGCTT AATTGTTCT TCCTTCTTAG CATTGCTG AGAAGCCAAA	50
25	CGTTGCGCCA ATTCAAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA	100
	TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT	150
30	TTAGGAAGTG ACGGTGTTGG GATACCACAA TCACTAGGTT CGGGAAATCA	200
	GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCAACATCCA GACCGTTGGT	250
	TCGA	254

35

(2) INFORMATION FOR SEQ ID :801:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 203 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

402

(xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5	ATCCAGGCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA	50
	TTTAACCACA CATTGCAACA AACTCACATT GGTTCCGAG CGGCAGTAAT	100
	AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT	150
10	AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA	200
	ATG	203

15 (2) INFORMATION FOR SEQ ID :802:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

	GACACAAC TGTTCACTAG CAACCTCAAA CAGACACCAT GGTGCACCTG	50
	ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG	100
30	GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG	150
	GACCCAGAGG TTCTTGAGT CCTTTGAGGA TCTGTCAACT TCC	193

35 (2) INFORMATION FOR SEQ ID :803:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :803:

	AACAAAAGTT GAAAATTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA	50
5	AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC	100
	AATAGCGTAC AGATTTTCC GCATTAATCC GTGTTTATAT TAACAGATTG	150
10	GTAAAGTATC GTTTAAAAAG GGAGAGAGGG GATAACCCTCT CTCTAGATAA	200
	ATGGGTCAATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTTCTAAA	250
	CGATAACAAG AACCCCAGTA GGTAGTATAG CAGTCTTTAA	290
15	(2) INFORMATION FOR SEQ ID :804:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :804:

	AACTTGATGG TCGAGGCCAT CTCCCTGGGCC GCCTGACGAT ACCGTGGCTA	50
30	AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC	100
	AACATTTCCG GCAATTCTCA CAGAAACAAG TTGAAGTACC TGACTTTCT	150
	CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCCCTAC CACTTCCGGG	200
35	CCCCCAGCCG CATATTCCCG CGGACCGTGC GAGGTATGCT GTCCCACAAA	250
	ACAGGG	256

40 (2) INFORMATION FOR SEQ ID :805:

(i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :805:

10	AGCAACCTCA AACAGACACC ATGGCGCACC TGACTCCTGA GGAGAAAGTCT	50
	GCCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA GTCGGGCGCG	100
	AGGCCCTGGG CAGGCTGCTG ACCGATTAC CCTTGGACCC AGAGATTCTT	150
15	TGAGTCCTTT GAGAACATGT CCACCTCTGA TGCTGTTATG GGCAACCTA	200
	AGACGAAGGC TCATGGCAAG AAAGTGTTCG GTGCCTTTAG TGATGACCTG	250
20	GCTCACCTGG ACGACCTCAA GGGCACCTTT GCACAC	286

(2) INFORMATION FOR SEQ ID :806:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|--|
| 25 | <ul style="list-style-type: none"> (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
|----|--|

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :806:

	TTCTTCATCA GATTTTACAT CTGCCTGATT AGAACATCTCT ACACCTGGCCT	50
35	CAGAAGATGA TTGTTCAAAA CTTTTCTAA GTTGCTGTAA AAAAACTTCC	100
	ACGGACAAAG TAAAATGCAG TTCTTTATCG TTTAGCCAGT GTACAACAAA	150
40	AGGTCCAATC TTCTCTTCAT TTTAATTCAAG ACTCAGAGAT GTAATAGATG	200
	GAAGAAGTGA AATGTCTGTG GCTGGGTTGA TGCTGGCTGC AATATGAAAG	250

405

TGGCAAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C

291

(2) INFORMATION FOR SEQ ID :807:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :807:

15.	AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTTATTAG GCAGAACATCCA	50
	GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG	100
	GAACAAAGGA ACCTTTAACCA GAAATAGAAC ACAAGAAAAG CGAACTTAGC	150
20	GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCCAC TTTACGATAG	200
	GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC	250
25	ACAGACCAGC ACGTCGCCCA GGAGCC	276

(2) INFORMATION FOR SEQ ID :808:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :808:

40	GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT	50
	CGATTCTAAA TAGACCTTT TACCAAGTCGC TGAAACTCTT AAATTAAGTA	100

406

ACATCGCTAG CTAATTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG 150
AAGCTTGTTC TTCACACGTT TCCCTTCAGG TCCTTGATG AATCATACTG 200
5 ACGTGATCGC TTATCGTA 218

(2) INFORMATION FOR SEQ ID :809:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :809:

20 AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA 50
CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT 100
TACTGCCCTG TGGGCAAAGG CGAACGCGGA TGAAGTCGGC GGCGAGGCC 150
25 TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC 200
TTTGGGGATC TGTCCATTAC TGATGCCGT A TGGGCAACCC TAAGGCGAAG 250
ACTAATGGCA AGCAAGTGCT AGACGC 276

30

(2) INFORMATION FOR SEQ ID :810:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

	GACTCCACCT GAACGGGCC CTTCTGAACC GCCTCTGTGG GAGCAGGCC	50
	CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTCCTTCT	100
5	GAGGAGGCTT ACTGCTTTC TTACTCGATT TATTTTCAG AGTTTTCTTC	150
	TTCGTACTTT TTTTAACGCA AGTATTTGC TTTTTATTCT CCTCCATTT	199

(2) INFORMATION FOR SEQ ID :811:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :811:

20	AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA	50
	AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC	100
25	TGGGGGGCTT GGCGTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA	150
	GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT	200
	TGCACCACAA TTGACACACAA CACACCTCAA AGCAGAATCC GCACTGACCT	250
30	AAGT	254

(2) INFORMATION FOR SEQ ID :812:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

408

(xi) SEQUENCE DESCRIPTION: SEQ ID :812:

	TTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA	50
5	CGCTCAAGGC CTTTCACACAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGAA	100
	CCAAGGACC CTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA	150
10	CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCACTTC CAAACAGGCA	200
	ACCTGCACCG GAGGGGAGAC TTTTCGCCA AAGCGACGGG CCAGCACACAA	250
	GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA	284

15 (2) INFORMATION FOR SEQ ID :813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

	ATACAACAGC AGAAACAGGT ATCCACGGCAC AGTCCAGCAA CATTTCCTCT	50
	GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATAACCAAA	100
30	GGCAAGGATG CTAACTCGAA GTCAATCACG CGAGTGATGT CATTCAACAAAC	150
	CGGTCAACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG	200
35	CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAAAG AGCTAGACGA	250
	CTGACGAAAC CTGAGAACCC CGAAGGACT	279

40 (2) INFORMATION FOR SEQ ID :814:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 base pairs

409

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :814:

10	AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCA	CCCC 50
	ACCAGTGCAG GCTGCCTATC AGAAAAGTGGC GGCTGGCGTG GCAACAGTGA	100
	CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGGAGC AGTGGCGACG	150
15	GGCGTGACAG CAGTAGCCA GAAGACAGCG GAGGGAGGCAG GGGGCATCGC	200
	ACCA	208

(2) INFORMATION FOR SEQ ID :815:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 192 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :815:

30	AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG	50
	CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG	100
35	TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCCAC	150
	AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA	192

(2) INFORMATION FOR SEQ ID :816:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 264 base pairs	

410

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :816:

	GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG	50
10	CCGCCTGGGG TAAGGTAGGC GCGCACAAATG GCGAGTATGG TCGCAGAGGC	100
	CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA	150
15	CACTTCGACC TGAGGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG	200
	GTGCCCGACG CGCTGACCAA CGCCGTGCCGC ACGTGGACGA CATGCCAAC	250
20	GCGCTGTCCC CCTG	264

(2) INFORMATION FOR SEQ ID :817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :817:

	ACCTTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAA	50
35	AAAACCACTC ACAAGCAAA CAACCCATCC TGTTTCATA ACGTTATCGT	100
	AAC AAAG CCGACCATAA TCAACTTGAA TTTACTTCAC CACAAGGCAA	150
	AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA	200
40	TG	202

411

(2) INFORMATION FOR SEQ ID :818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :818:

AGTAGAAAAT AAGTTCAAAA TTTAGAAAT ACTGGCTTTA TACTCGCCCA	50
TGTATTTACA TTCACAGAGA TCTTTATTAA TTTACAAGCG CTTTGAGTTA	100
CTGTATAGTT TTTTTAACCA AAAAAGCGTG GGGGGCTCCC TTTAGCATTC	150
CCCATAGGAT AGGTAATGAA CTTTTGTT	179

20

(2) INFORMATION FOR SEQ ID :819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :819:

TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAAACT	50
AATAGCATAG GAGCATTAA TAATACGATT CGATAACAAA AAGAATTAA	100
GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCAAT ACTGATCTAT	150
CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAACG GATCAAGTTG	200
TACGCCGGTC CACGAAGTGA CAGACGAAAA ATGAACGCAA GCTGATGTAA	250

412

ACGCATCACA

260

(2) INFORMATION FOR SEQ ID :820:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15	ACTCGGCACT TTCTTAGAAT AGACAATTG CAAAATGTCC ATCCCAGGTT	50
	CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG	100
	TGAACTTTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC	150
20	ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC	200
	TTTCCGTAAC TGAGTTTGAT TTCTCC	226

25 (2) INFORMATION FOR SEQ ID :821:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

	CACCTACATA TAGATGCACG AAGTACTTGC TCACTTTTT TGGTTGTAAA	50
	TTTCAAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA	100
40	GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTTCGCATCGC	150

413

G TGATTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC 197

(2) INFORMATION FOR SEQ ID :822:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15	GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTAT AGCTAGCAGG	50
	GTAATGGGAA GTTATGGCAC TCAGGTACA TTCTAGGGAA TGTTTATCGG	100
	GCAATCTCAA TGGCACCGCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT	150
20	TGCGCTTCT TCATCGAAC CTTGCCAA GACATCTGTT TTTCTGGAT	200
	CACCCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT	250
25	AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA	300
	CATG	304

(2) INFORMATION FOR SEQ ID :823:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :823:

40

GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTTG	50
--	----

414

GAGGTCA	GCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCCA GGGAGGCCGTG	100
CACCAANGGG	GCGAACTCNC GGGGAGGCAGG GCGACCAGGG TCACCAGCAG	150
5	GCAGTGCTTA GGAGCTGGGA GCCGACCGAG CCCACCGAAC TCGCGCG	197

(2) INFORMATION FOR SEQ ID :824:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :824:

20	AAAAACAATG TCATTTGTA CAGACAAAAT TTAGCAGACT CAAGCTTCCA	50
	CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT	100
	GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCTGACT TACCCCTGGCA	150
25	GCTTGTGTT CCCACATTAC TAGTAATGTT TTTTCCTTA ATAGCAATGA	200
	TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCAG ACAGCAAGCG	250
30	TTTCCCACA GGTCTCGACA CACAGAAAGAT A	281

(2) INFORMATION FOR SEQ ID :825:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

	TATTAATTT ACTAGAATGT TACAGTTACA AATTTGGTAA TGTTCTTCT	50
	GAAAAACAGC CTAATTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC	100
5	TTTATTCCAT GATAGAAAAA TAATTCTGG CTTCATCTCA CAATTAACTA	150
	ATAATTATGT TAATATAAAA TATAACTGTG CCCTTTCTT TCAGTGATGA	200
	TCAAAGTGAT TCTCCCAGGC CAAAAAATCA AATAAGAAGT TATATTTAA	250
10	AAAGACATAA CAAGCCATTTC TACCCAGTGG GCATCTTCAG TGTACTCCCT	300
	CTACTAATTG GC	312

15 (2) INFORMATION FOR SEQ ID :826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

	ACACCAAACA CGGGGACTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA	50
	GGGCAGGGAG GGGAAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA	100
30	TCCCCAAAGCC CTAGAGACCC CTTCACTGCA GCACCTGCC CCGGGTCTCA	150
	GGCAGCTTCA GGGCCAGAGA GCTGCAGAGG GCAAGCAAA	189

35 (2) INFORMATION FOR SEQ ID :827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

416

(xi) SEQUENCE DESCRIPTION: SEQ ID :827:

	CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT	50
5	ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAAG CTATGAGTAA	100
	AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT	150
10	TTAGAGATTA TTTTGTTGCC TGGAAATCTG TCTCATCACA GAGTGTAAAT	200
	ATACACCGGC GGGATATTCA AGAGTGGCTA AG	232

(2) INFORMATION FOR SEQ ID :828:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 282 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :828:

25	GGACATTGGA ACACATATACT CTATTATTGC GGTCGTGCCT AGCAGTCTCG	50
	CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT	100
30	TATATGCGCA GACCCGAGA CTGGGAGACC CAGACCCAGG GCAAACCTCTC	150
	TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT	200
	CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA	250
35	GTAATTACCC CATATCATAA AATGGGGGGG GG	282

(2) INFORMATION FOR SEQ ID :829:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 230 base pairs
	(B) TYPE: nucleic acid

417

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :829:

	CACTACATCC GCAAGTACAA CGCGTTGAG AAGGCCACA AGAACATGTC	50
10	TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA	100
	AGTGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCCTTC AACGTGCTCA	150
	AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCCAGAA GTTCTGAGGC	200
15	TGGACATCGG CCCGCTCCCC ACAATGAAAT	230

(2) INFORMATION FOR SEQ ID :830:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 226 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :830:

30	TTCCGCAAAT AAAAGAATTG ACTAAGGTAC CAAAACAGAA AATATAACAGA	50
	GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAAG AGATAAAATG	100
	GAAGAGAAAT GCTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA	150
35	TAAACTTAAC AAGAAATGTT GCAAAACCCT TATGTAAAAA TTACAACACT	200
	CCTGAAGACG CAGACACACC TAACAA	226

40 (2) INFORMATION FOR SEQ ID :831:

(i) SEQUENCE CHARACTERISTICS:

418

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :831:

10	AGAAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC	50
	CTTTTCCCTT CTTTTCTACA GCCTGCAGTT CATTAAAGGA TCACCGGAGA	100
	TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG	150
15	ACCCCTGAATT TGGCCCAAAT TTGTAGAAC ATTGCTTTT ACCACCCGGT	200
	GCACCAAAAA TACCTCCCCT TTCAAGGCAA CAACCGCTTT AATTGCT	247

20 (2) INFORMATION FOR SEQ ID :832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :832:

30	CACCAGGCAG GGGATCCCCG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG	50
	GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT	100
35	GGGCAGCAGG AG	112

(2) INFORMATION FOR SEQ ID :833:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid

419

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :833:

	AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA	50
10	ATGTTCATCT CATAACTCTC CTCCCAGCAG TGCACCAGTA AACTCAGATG	100
	CCTGAGTGCT TGTGGCCACC ACACAACAGA TGCGGCCTTC CTCTTCACTG	150
	GCCCCCTCGGC TGCTGCTGGG TCC	173
15		

(2) INFORMATION FOR SEQ ID :834:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :834:

	TGGCCCATGG GAGCCTTAT GAGCAAGTTT CCAGGTCCCT ATGACACAAT	50
30	TCCATCATTC TTCGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTT	100
	CAGACTTATC TTATATTTTC ACTTCCCCAT ACCTGGAATC AATCACTTCT	150
	CCGAGGATGC TTGATTCCCTT TTAGTGAAGA ACAGTCTTTG GAAACCAACC	200
35	GTCTAGGGAC ATCAAGTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG	250
	AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT	288

40

(2) INFORMATION FOR SEQ ID :835:

- (i) SEQUENCE CHARACTERISTICS:

420

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :835:

10	CTTTTCTATT TTCCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA	50
	GTACAAAAGA GAGAAATTT AAAGCTGGGT GTCCGGGGGA GACATCACAT	100
	GTCCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAAACCAG CAAGTTTTA	150
15	TTAGTGATTT TAAAAGGGGA GGGACTGTAC GAATAGGGTG CGGGTCACAG	200
	AGATAACGTG CTTCACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA	250
20	GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA	300
	ACGTCTAGGG	310

(2) INFORMATION FOR SEQ ID :836:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 177 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
30	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :836:

35	TCAGTGGAGG AATTAAAATC GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	50
	GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	100
40	GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTAA	150
	CATCTCCCAA AATGCCTAGC ATTCTTC	177

421

(2) INFORMATION FOR SEQ ID :837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTCTGGC ATTCTGCAGG GCGGCACCTCT CCCACTCTTC	50
15 CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGCACAA	100
TGTTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT	135

20

(2) INFORMATION FOR SEQ ID :838:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :838:

TCAGTGGAGG AATAAAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	50
35 GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACAA	100
GAGGTAATCA AAAACTCGAG CATGTATTC AGGATCCATG ATTGAATTAA	150
CATCTCCCAA AACGCCTAGC ATTCTCGCC ACATTACAGT AGCAACATCA	200
40 G	201

40

(2) INFORMATION FOR SEQ ID :839:

422

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10 TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA 50
GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCTGAGA 100
15 TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT 150
CTGAGATGTA CACGAACGAG ATCTTTGAG A 181

(2) INFORMATION FOR SEQ ID :840:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30 CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG 50
TTTTAGTGAA CATTCAAGAGG AGTTTCCAAG AAAGTCGCTG CACAATCTTC 100
35 ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA 150
TGTGAGTAGA AATGGCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA 200
TAATAACATG GGTTTAAAAA AC 222

40 (2) INFORMATION FOR SEQ ID :841:

423

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10	CGCTCAGCTG GTCTATCCGT CTCTTCCTCT TGTCCCTTGCT CTTGCTGCGG	50
	CTCCTATCTA CCGGCTACCT GCTGCCCGCT TTGCTCCTGC TACCGGCTCC	100
15	GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCCTGCT CACAACCTCCC	150
	TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTGC	200
	TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT	250
20	GTCATTGTTT TGGAACTTCT CCTTCAGCTT GGTCTTTGC CGG	293

(2) INFORMATION FOR SEQ ID :842:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 239 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35	ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC	50
	TGGGATAGGT GTCTCATTAA AATCTCATAA TCATCTTTTT TGGCAGGTCA	100
	GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCAAA GACACACAGG	150
40	AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC	200

424

TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAAAA

239

(2) INFORMATION FOR SEQ ID :843:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15	TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTC	50
	AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA	100
	CTCACTCACT CTATAATAAA ATGTTGCAC TCAATTATA TAGTAGTGT	150
20	TGTC	154

(2) INFORMATION FOR SEQ ID :844:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35	GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG	50
	CCAGGAGTTG GGTGGAGACT GAGTGGGTT TGTGTGGGTG AGGGGGCATC	100
	TACTCCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC	150
40	TGCCTTGGAG CCTTAGTCCC TCCCTTAGGG CCCCTCAGC CTACCCATAC	200

425

CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCACTAG CAGGTTCCCC	250
ATCTTTCCA GGCTGCCCT AGCACTCCAC GTTTTCTGA AAAAATCTAG	300
5 ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTTGT GAGCTGTAAG	350
GTAAAGCAAG TTCTATCAA TTAGAAGCTG TTGGGGCGT AT	392

(2) INFORMATION FOR SEQ ID :845:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :845:

20

CAAAGAATAA ATAATTTTC TATTCTGAA AGTTAACTAA TTATTTATTA	50
GAAAGTCAGA AATATGTGGA AACCAAAGGA ATATTTGAGA AAGTGATATG	100
25 AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTTCCTTT	150
GAGCTAATCC TTTATTTATT TATTTTTTC CTTGAGACAA TGTCTTGCCA	200

(2) INFORMATION FOR SEQ ID :846:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :846:

40

TTAAAAATAC TCTGGAAAGA GCACCTCCAT CGTTCATTTA CATCATATTA	50
--	----

426

	GAAATGGATT TCCGAGTCAG CACTGCCCTTC CTCCAGAATA GCAGTCCTGG	100
	AGGAGCGAGA TCTCCCCAAG CCTCCAGGAT TGCAGTCTGT TTGTGCCTT	150
5	CACTCCCTAA TAGGTTTGCC TTATTTAAAG GACCCACCTT CAGAGCTGCC	200
	AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC	250
	ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAAGC CTAGGAGTAA	300
10	GAGGAGGTGG T	311

(2) INFORMATION FOR SEQ ID :847:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 287 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :847:

25	CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA	50
	CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTGCC	100
	GGCAGGAACG TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC	150
30	CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG	200
	GCAGCTCGAG GCCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG	250
35	CCCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT	287

(2) INFORMATION FOR SEQ ID :848:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

427

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

	GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAC	50
10	TCATCCATAC GTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA	100
	TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATTT ACCTATCGAG	150
	AGGCATCTG ATTACTCTA GCTTGATT ATTACAAATA AAACTATACA	200
15	AACACGCAAA CAGAGTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG	250
	AGGCATATNA CCA	263

20 (2) INFORMATION FOR SEQ ID :849:

- | | |
|----|-------------------------------|
| 20 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 279 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 25 | (D) TOPOLOGY: linear |

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :849:

30	TTGTCAGTCA GAATAGGATG TAAAAGACTA TTCAAAGAG TTAAATTATT	50
	TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG	100
35	CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT	150
	TGACATTAAA AACGAATGGA TACCCAACTC TGAATTCCAT ATCGTTTTT	200
	AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA	250
40	GTTTATCGAA ATCCTGCCGC TACTAAACA	279

428

(2) INFORMATION FOR SEQ ID :850:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :850:

GCTGAAAGTT	GAAGTGGAGA	GCTTGAAACG	AGAACTCCAG	GACAAGAAC	50	
15	AGCATCTGGA	TAAAACATGG	GCTGATGTGG	AGAATCTAAA	CAGTCAGAAT	100
	GAAGCTGAGC	TCCGACGCCA	GTTCGAGGAG	CGACAGCAGG	AGACGGAGCA	150
	TGTTTATGAG	CTCTCGACAG	AAT			173

20

(2) INFORMATION FOR SEQ ID :851:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :851:

TCGAGAAAGT	TTCAATGTGA	TTAGATTTAA	ATTAAAAAGAA	TCCATAAAAA	50	
35	TGGAACAAAG	AAGAAGAGGA	ATGAAATTAC	TTTACTTTA	AACAGCATTG	100
	TTATCACATA	AAACACGTAT	CTTACAAATT	CATGGGATAG	CCCATAATG	150
	GGACTACAGC	AACAATGGTA	GGAGAGTCCA	TCCTTCTTCA	AAAGCAACCC	200
40	AGCAGGAATT	TTCTGTTAAA	AATATTTTG	CCGTAATACT		240

429

(2) INFORMATION FOR SEQ ID :852:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :852:

	ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGGAATGTTA	50
15	AAGGAATTTC TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC ACAACATCT	100
	GCTTATTATG AAAGTGTGTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC	150
20	CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAAACG CTTCTGCTTA	200
	TTCCTCTTAT AAAACAAGGG CAATTTGTG AGAGCTACTG ACGATTTCC	250
	CCTCGAAATT TACTATTTCT ACAGCTTATT AATCTCAAAT AGTAAGCATG	300
25	TCCTTGCCGT CACT	314

(2) INFORMATION FOR SEQ ID :853:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :853:

	TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTAACCTT ATAGATAGCA	50
40	CCAGATATGA GTCTTATTAA GTTCTGATAA CTCTGAAATG GTTATTTGGT	100

430

ATTTCTTCAG TGACAAGCAA ACTATCCCC CACATGCCTT TAATGGCCAG	150
TGTTTTCGAT TTGTATAACCA ATAAGCAATC TAGGTAGAGG TAATCATATA	200
5 CTGATACGCT AACCTTGAA ACATAATTTC CAATCTAGTA AGCTAAAATC	250
GCGCCAATAC TGCTTAA	267

(2) INFORMATION FOR SEQ ID :854:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :854:

20

GCAGTGGATC TTTCTTTTT TCCAAAGGAA ATTCATATA GAGTCCATT	50
ATAGGAAACA GATAAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG	100
25 GCTTGGAGCC CCCAGCCTCT TTGCTTTCTC TTATCCSTAT AGGATGGCCA	150
TTAGGTGAAG CAGTTTAGCT TGTTGGTTCA GACCTG	186

(2) INFORMATION FOR SEQ ID :855:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :855:

40

ATTTTGAAAA GAAACCTACA AAAATTGTAT TTCCATATTT CATAAGTCAGC	50
---	----

431

	CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG	100
	GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT	150
5	GGCCCAAAAA TT	162

(2) INFORMATION FOR SEQ ID :856:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :856:

20	TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA	50
	GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT	100
	GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG	150
25	GAACAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC	200
	AACATAACAA ACCCAATCGC CCTGTTAACT TTAAATCTTC AACTCGAGAA	250
	AAAGGCTCAT GACTACTTCT AACCATGCCA AAACCC	286

30

(2) INFORMATION FOR SEQ ID :857:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

	AACTATATGG TATTATTTCA CGCTGTACCC AGTCCATTGC TTGAACTTAC	50
	GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTT	100
5	CCCCTTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG	150
	ATTTTCTTT TTTATAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC	200
	TTTAGAAAT GCATATAAAT GCTCTACGCT CCTTTTTCT GTTACTTAAT	250
10	CGGCGCCAAG GCCTTTACAT GAATACTCAG	280

(2) INFORMATION FOR SEQ ID :858:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 310 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :858:

25	CACTGGTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG	50
	GCCAGGCTGG TCTTGAACTC CCAGCCAACC TCAAAGTGCT GGGATTACAG	100
	CTGTGAGCAC CAGCCCAACC TCGCCTCTT AAAAAGAAAA AACACAAGTC	150
30	CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTACAT	200
	CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAARACAT	250
35	TATACAGGGC TTGAACGTGTC TTTTAAGCAA GCCCCAAATC CTTTGAAAGG	300
	AGGCAGTAAC	310

(2) INFORMATION FOR SEQ ID :859:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs

433

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :859:

10	TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG	50
15	CCACAGCAGG GCCCTCTCAG GCTGGAAAC TTCTGCCAGA GCTGGCGAGT	100
20	CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC	150
25	AGGAAGAG	158

(2) INFORMATION FOR SEQ ID :860:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 263 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :860:

30	TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT	50
35	CCAGGAAGGC ACTAATCAA GATGATATAC AGCCAGGTAA AAAAGAACAA	100
40	TTCACAGGCA CAAGACTATA TAACCATCGT TTTATTTCA AACGTTATAC	150
	AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT	200
	TAGATTCGGA ATAACCTGAA AATAAATCCC AACCCACGTAA CTTACTAAAG	250
	GAATAATGAG CCA	263

(2) INFORMATION FOR SEQ ID :861:

434

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :861:

10	ATTTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG	50
	GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAAACTG ATAAAAGATT	100
15	ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTTGT	150
	TGATCCCATA GGTCATTTGT TATTACTCTT CTTCAACAGA GTGATTTCT	200
	ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG	250
20	AAAG	254

(2) INFORMATION FOR SEQ ID :862:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :862:

35	GTTCCCTCCTT TGTAATTAT GAAATATTAA TAGTTAGAC TGAGTAATAT	50
	GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC	100
	CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGTCTGC	150
40	TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA	200

435

TCTTTCCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC	250
TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT	300
5 TCACCTACAC GTGGCTCGCT TTAGTTGCT GAGCAGC	337

(2) INFORMATION FOR SEQ ID :863:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :863:

TGGTGGGTTTC GAGCCCAACT TCAGCGCTCT TCGAGAAAGTG CGAGGCGAAC	50
20 GGTGCGGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC	100
TCTCAGCGAC GACGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA	150
25 ACTTACAATG CCACCGCGA	169

(2) INFORMATION FOR SEQ ID :864:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :864:

ATTAAGGTAA AGGAAGACTT TCCATTGTTA AGTAGAAAGA GTGTCCTGCT	50
40 ATTACTACCA TTCACATCTA GTTTGTGTGA ACTAGGGTTT TCTATCTTAA	100

436

	CCCTGTTAAA AACAAAGGAA AGAARTGGGC TGAATGGCGC ACCAGCTATG	150
	CGGATAGCAT TATCTTCCTG TGTTCCAGAC TGGAATGAAT TTATGAACAA	200
5	GGCAAGCACA CCATTATACT AAATAAAATC TTACCTAGTT TTCGTTTTG	250
	CATTTCTTAC TTCGCAGTAT TTCTCCGCC AAGAGC	286

(2) INFORMATION FOR SEQ ID :865:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :865:

20

	ATATAGTCGG CTAGGGATAG TGAAAAATTG GGGGCTTGGT TTAGATTGGA	50
	GAGGTATATG GTGGGGTGTG TC TTATAAGGCT TAACTTTGGG AGGGCCAGG	100
25	GCCTTGATTT CTGTCCCCCT TGCCTTGCCTT GGCCTTGAA TTGAAAGCTT	150
	TGAATTAGGC CTTCATAGAT TTTAGTGTGC ATACAAATAA CACGATCTT	200
	TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTC	250
30	GCATTTCTGA TCTATAAGGT GA	272

(2) INFORMATION FOR SEQ ID :866:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

437

(xi) SEQUENCE DESCRIPTION: SEQ ID :866:

	ATGCAGGAGA AGAAGGATGC CAAACTAAGT CAAAAAAACG GAACGCAAAT	50
5	AAAAGGAATG ACCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG	100
	GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG	150
10	CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG	200
	TTTCTAACAC TACAACGCTA ACTTTGGAA CGTATCTACT TCTAGCATGT	250
	AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG	296

15 (2) INFORMATION FOR SEQ ID :867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

	TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG	50
30	CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA	100
	CTGTGACTTC TACGATGAAA GAACAAGGGA GAGAAGATCT TATCGACAAT	150
	CATACAAAGC CATATATAACG CTATTCCTCA ACTCACAGAG TTAATTAAAT	200
35	GTCACCAGGA TGGAAGAAC CTTATAAGCC CCTATCTATC A	241

(2) INFORMATION FOR SEQ ID :868:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

	GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC	50
	ACGCCACTCTCACACACTCTCACACACGCA CCCTCTCGCG CATGCTCTCT	100
10	CAAAGCCCAA TATAACCAAG GGGAAAGGAAT	130

(2) INFORMATION FOR SEQ ID :869:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 310 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :869:

25	TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTTGAAAAA	50
	CTAATGAGAA TGGCATAAAC AACATTTAAG CAATATATT TGAAATTTAA	100
	TTCAAATGGT CAAATTCTG GAAAACACAA ACTCCCTTCA CTAACAGAAT	150
30	TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA	200
	TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT	250
35	TCCCAAGCAC TTAAACAATA ACAATGCC TCTTTATACA AACCTTCCCC	300
	AGTAATAGAA	310

(2) INFORMATION FOR SEQ ID :870:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs

439

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :870:

	AAAGAGGCCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA	50
10	TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC	100
	CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG	150
15	CAAGTGATGG ATTTAAGGCA AATCTTGTTC TTAAGGAGAT TG	192

(2) INFORMATION FOR SEQ ID :871:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 250 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :871:

	ACCATAGATG TGTTCCAGAG GCAAAAGAGA CACATTATCC TAGATGGCAG	50
30	AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCCAGAT CTTTCTACAT	100
	TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA	150
35	CTAGAGTTTC ATCCAATAC CTGACCACGA CTTCATGGAG ATTTGAATAA	200
	TCTATCCGAT GAGATTATA TNTAAACAAAC TCAACTCCTG TCGAAACAAA	250

(2) INFORMATION FOR SEQ ID :872:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 313 base pairs

440

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :872:

	TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA	50
10	AGGATTTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCCAGAGAT	100
	ATACCCACCA ACAGCCCAGA GCTGGAGGAG ACACTGACTC ACACCATCAC	150
15	AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG	200
	TGAAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC	250
	TTCGTGGCCA GGGAAACACA TGTTCCAAGG AAAGTAATGA AGAGTTGACC	300
20	GAAAGCTGTG AGA	313

(2) INFORMATION FOR SEQ ID :873:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :873:

35	TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG	50
	ATGGTAAGAA AAATGAAAGA CACACACAAT GAAGAAGAAA TTAGAGAAC	100
	ATTCCGTGCG TTTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC	150
40	TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT	200

441

GATGAAATGA TCRAAAACGT AGATNATTGA TGACGATGGT AAGGTAAACT	250
ATCCAGCGTT AGCACAAATG	270

5 (2) INFORMATION FOR SEQ ID :874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTTC ATCTCCAAAG CCAGCCATGG TGTATTTCTC	50
TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT	100
20 GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT	150
TAATGACAGC TGATTATTC CATCTGAAA CTTACTCAAG AATGCAATCC	200
25 AGACTAACAC GACAATAGGA CATCAAGCT	229

(2) INFORMATION FOR SEQ ID :875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :875:

TTTGAACTTT CAGCCGAATA CATCTTTTC CAAAGGAGTG AATTCAAGGCC	50
40 CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTCT	100

442

	TGGTCTTGAC CAGCCTCTCT CATGCTTTG GCCAGACAGA CATGTCGAGG	150
	AAGGCTTTG TGTTCCCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA	200
5	AGCACCGTTA ACGAACCTC TCAGAACCTT CACTGTGTGC CTCCACTTCT	250
	ACACGGAACT GTCCTCGACC CGTGGGTAAC AGTATTTCT GCGT	294

(2) INFORMATION FOR SEQ ID :876:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :876:

20	ATTTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG	50
	TAACTAACAT GAAACCACAG AACTGTAACCT CTGCCACAGC TGCACTGAAC	100
25	CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCCAGAGCT	150
	ACGCCAACAA AAACCGTTAT TAA	173

(2) INFORMATION FOR SEQ ID :877:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :877:

40	TAATCAAAAG AGCTCTAAAT CTGTAATTTC TTTCTCCTTT AAAAAAAATGT	50
----	---	----

443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG	100
AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTCG AAC	143

5 (2) INFORMATION FOR SEQ ID :878:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTTCA G TGGTTCCCTGC TGTGGGACTT	50
20 GCGTTTCAC TAAAGTGTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC	100
AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCCTGGA ATGAGGCCCA	150
25 GGGCTTCTAT TGCTAATGCC TGTAAACCTT GCTGAATCTA TAACAGAGTC	200
TATACCGCTC TCG	213

(2) INFORMATION FOR SEQ ID :879:

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTAA	50
40 ACCAGATAGA CACATGCTTA TTCAAACAC AGATATGATC CAGTTAAC	100

444

CCTTCTTAGA ATGTGCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT	150
AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC	200
5 TACCAAGAGTA ACCGTCATCC CCTTGAG	227

(2) INFORMATION FOR SEQ ID :880:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :880:

ATAGACAAAG TCCTTCCCAC TAGAACATTAC ATTCCAGTGG GAAGAATTAG	50
20 AAGCCTCAGG AATTCCATTG CTTACTTTA GTTGTTACTT CAAAAGTACT	100
TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA	150
25 TCCAGGGCAC AGTATGTGAA TTGTGTTCG TTCCTTTAGG AAAAGGAAAAA	200
ATAATCACTC TTTACAAGGT A	221

(2) INFORMATION FOR SEQ ID :881:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :881:

40

AATTGTGGTA TATTCATT AAAATCGATC AAAGACAGCA ACATACATTA	50
--	----

445

	ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTAA AACAAAGATT	100
	CATATTAAAA CAATGATAAG TAATACTTAG AACTGCATC CTAGAGACAC	150
5	ATCATTGCCA TTTTAGAAA AACAGAAACA TATTAGTGTG AAAAGATGTT	200
	AAAAAATGAA TATTAACCG TCGAGCACAA CACACTACGC CGATAACAAT	250
	ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCCTCGT	300
10	GGCGATCCGA	310

(2) INFORMATION FOR SEQ ID :882:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :882:

25	GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT	50
	GGAGAAAATG GATCTATGCC GATGTCGTGA CACACACACA CACACACATA	100
	CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA	150
30	CGAACTACAA ACGTAACAGC AGCAGGC	177

(2) INFORMATION FOR SEQ ID :883:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

CAATTCTATT TTCAGAGTTG ACTGTACTCT TTTCTCTGA AGATACACGT 50
5 ATAAACCGGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA 100
ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC 150
10 GA 152

(2) INFORMATION FOR SEQ ID :884:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :884:
CCATAATATA AGTATTATTC ATGTATTCTG TGTCTGGAAT ACAATTCAAT 50
25 GACCTATTTC AGAAAAATCT TTTCAAGTAC TGGCTGAAAG ACTGAGGGAT 100
ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA 150
AAATGAAATT GTGCCGAAAT GTATACA 177

30 (2) INFORMATION FOR SEQ ID :885:
(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

	CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAAT	50
	TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TTAACTAGAA	100
5	TTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGAGT	150
	GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTAA CAAATATATA	200
	TATTAATAT ATATATGTT TATAGAAACA CAGAGCACAC A	241

10

(2) INFORMATION FOR SEQ ID :886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :886:

	GTAGCAACCG GCGCTCAATA AAATTCAACC AGCRAACTCG ACAAGTAACA	50
25	ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA	100
	ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG	150
	CCATCCATAT ACCAAAAATG CTACTTACAA CACCACAACA	190

30

(2) INFORMATION FOR SEQ ID :887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

CACGCTTCT	CTCACACAGC	ACTAGCGCTC	TCTCACTATC	ACTCTTCTCA	50	
CAGAGCTGCG	CGCGAGTCTC	ACTACTATCA	AATATATCTG	TCTCTTCTCA	100	
5	CTCTATAGCT	CTCTCACAGA	TATATATCTA	CATATAGCGC	TCTCATTATA	150
	CTATAATATT	ATACTCTC				168

(2) INFORMATION FOR SEQ ID :888:

(xi) SEQUENCE DESCRIPTION: SEQ ID :888:

20 ACTGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT 50
GCCGATCTCG CAACCGGTTC CAGTTAGACA GAACATTGTG ATATTCAAAC 100
25 CACTTTCTCG TAATTTCCAA TGGAGTTGTA AAGTTTAATG AGACCTCGAT 150
AATCATATTC TAGTCCACTG TAGC 174

(2) INFORMATION FOR SEQ ID :889:

(xi) SEQUENCE DESCRIPTION: SEQ ID :889:

40 AGACCCAGACT TAAGGAATGG GAGTTATATT TCACCTCCCT GAGGCCAGAA 50

449

	TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA	100
	TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT	150
5	ATATGTGTGT GTACAATATA TAAAAAAATTA TATGGGAGAA AAGAAAGGCA	200
	AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTG TGTGTAACAA	250
	AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT	300
10	ATATATATAT CTGTATATAC AGGTATA	327

(2) INFORMATION FOR SEQ ID :890:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 181 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :890:

25	TTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC	50
	GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC	100
	TCGCTCTCTC CCGCGCGAAG ATCTCACCCCC CGCGCGCTCG CGCGATATAT	150
30	ATCTCCTCGC GCGCGCGCCG AGCGGCCCG T	181

(2) INFORMATION FOR SEQ ID :891:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 207 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

450

(xi) SEQUENCE DESCRIPTION: SEQ ID :891:

	CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCCTCAC	50
5	TCTCAGGGGA GGGAGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT	100
	TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTT GGCAACCCAA	150
	TTCACAGTTT TGTAATTTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG	200
10	CAAAGAA	207

(2) INFORMATION FOR SEQ ID :892:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 198 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :892:

25	CTATCACTTC AGGGAAACAA ACAACTAACAA GCCATCAATT CAGAGGGAG	50
	TGATTTACA GTAGAGTGAA CGAAACTTGG GAAGGAAAAC ATCCAAGAGG	100
	CGTCTGTTG ACGTGGGTAA CGTGGGAAC GCATACTGTC TGGCAAGAAT	150
30	TCTACTAGGA CCACGGAAA CAAAGCAGAT TAAAACACTC TCTACTCT	198

(2) INFORMATION FOR SEQ ID :893:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 96 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

451

(xi) SEQUENCE DESCRIPTION: SEQ ID :893:

	CTTTAGAGAA TGCCTTGTGG AAAAAAAA AAATGGGCC CAATACTTT	50
5	TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG	96

(2) INFORMATION FOR SEQ ID :894:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :894:

20	AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA	50
	ATGGAAACAG CATAATACTA CATACTATCG CGCGGGTTG TCGGCGTGGT	100
	GGGCGTGCCT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA	150
25	GAGTGAGCGT GGGAGGGTGT GGTCGGTGGA GGTGTGTGGA GAGGTGAGTG	200
	TGCGAGAGGG GCGAGTGTAT GTGTGATAAG TATAGCGCGC AAGAGGGCAG	250
	GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAC	300
30	AATAACCACT ACTCACATAG AATAT	325

(2) INFORMATION FOR SEQ ID :895:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

452

(xi) SEQUENCE DESCRIPTION: SEQ ID :895:

	ATAGTTGTAC ATTTTATGG GGTGCATGTG ATATTTGAT ATGTGCATAC	50
5	AATGTGAGC AATCAAATCA GGGTAATTGG GATATTCAAC ACCTCAAACA	100
	TTTATCATTT ATTTGTGTTG GAAACATTCA AACCTTTCT TCTAGCTATT	150
	TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTTGTGAAT	200
10	AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTGAT ATACTGATTT	250
	TCTTTCTTTT GTTATA	266

15 (2) INFORMATION FOR SEQ ID :896:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :896:

	AAGAAGAGTC TTCTGCACAA ACAAAACCAT AGTGTGACA AATAGTCATG	50
	GCCAATGGCA ATCTGATGGT CCAGCGGCC CCGGATGACT CCTCTGCAAG	100
30	GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAAACT	150
	AGCAGGGCCC GAAGACCCGCC CGGCCCGGCA TGCCCTGGCG CAGGGCC	197

35 (2) INFORMATION FOR SEQ ID :897:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

453

(xi) SEQUENCE DESCRIPTION: SEQ ID :897:

	GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT	50
5	GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTTGTGAA	100
	TATTTTCCTT CCGACTAACT CGCGCCCCAC TCTCTTGCAGA GCACAAACAC	150
10	ACGGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT	192

(2) INFORMATION FOR SEQ ID :898:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 224 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :898:

	TGGATGTTT CATTGCAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC	50
25	TTGATAGAGT TGGCAAAATT GAACTATGAA GTTAACTATT TAACTCAAGG	100
	AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTT	150
30	ACATTAGAAC TGACACTGAA AACATAGCTC TTTTCAGTC CACCCTGGTT	200
	GCTCTAGTAG CCCACAGCCC AATC	224

(2) INFORMATION FOR SEQ ID :899:

35

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 362 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

454

(xi) SEQUENCE DESCRIPTION: SEQ ID :899:

	GAGGTGATTT CTCAGAGTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG	50
5	TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA	100
	AATGCCAAAAT ATTCTAATGT TTCAATGTT TCACATGAACA TATAGGGAG	150
10	CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC	200
	CGAGTCTGGC TACTTTCTAG GTAGTGTGCT TTTTGTCAA TTATAAAAGAT	250
	ATATTCCCTT TGTTTTTGAA AACCGAGTGA GATGCTTAAA TAGAGTACAA	300
15	TTATCTCATT CAAAATGTAT GTTGTTCCT CTCGAGAATT GTGAAGGTT	350
	TGAGATTGAA TT	362

(2) INFORMATION FOR SEQ ID :900:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :900:

30	GTATGTAGCC CAGTGGGTGT CTTCCCACAG GGTAGGTACT CAGTTGCTC	50
	TGGAGGGTGA CTCATACCTA AACAAAGTGA CATCTCCTTT CTCAGTAAAG	100
35	CCAAAGCAGG TTTCTACATT TGGAACAAAA GAGATCCTGA CCAGAGAGCT	150
	ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACCTAGAA	200
	AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA	250
40	AGGGAATGAG ATTGAATGTT ATTTAAGGGA TATTCTGTC AAGTTTGTT	300

455

TTCTCGATGA 310

(2) INFORMATION FOR SEQ ID :901:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15	TTCCCCCATG AGACCGTTAG TCTCTCTTG CCTGGCTGAC TACCTGCATA	50
	CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGACTCCTCC AAAGATTGCA	100
	GGGGGCGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTGGCCC	150
20	CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA	185

(2) INFORMATION FOR SEQ ID :902:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35	ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCCTAT TCTCCTCCTG	50
	TCAAACAACT AAACTACTCC GATGTTGAT GAAAATTAAA CTGCTACTCA	100
	GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCCAGG GAGGCTATTA	150
40	CGTGTGACCT TTGAGATGGA CCTGATGCC CCTTTTACTT TTTAGACTAC	200

456

AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAACTCCTG TAAAGAGTAA	250
GAATATGGAA AGGATGAAGC CTCATTCATT CGGGCATATT AAAAAGAAAT	300
5 TGCCTTCAGA AACACTTTGC CTTTTAATAT GTGTAGCTAC AGTAAGTACC	350
AATGGGCTAA CTAATTGAAG CTAACATTT A	381

(2) INFORMATION FOR SEQ ID :903:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :903:

20

CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAAACTG ACATATGTAT	50
ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAAGTCCAT GAATAATAGC	100
25 CTCTGCGCTG TTGCGGGTCC TGCAGGAAGTC CTCGGAGCGG CCGTCGCGGA	150
AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC	200
ACTTTTTTTT TATCGGCACC AGGCCCGTTC CTCCCTCCTCC	240

30

(2) INFORMATION FOR SEQ ID :904:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

	CCCTGGGCAG GCTGCTGGTG GTCTACCCCTC GGACCCAGAG GTTCTTTGAG	50
	TCCTTTGGG GATCTGTCCA CTCCTGATGC TGTTATGGGC AACCTAAGG	100
5	TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCCTTAGT GATGGCCTGG	150
	CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA	200
	CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTTCAGGCTC CTGGGCAACG	250
10	TGCTGGTCTG TGTGCTGGCC CATCACTTTG	280

(2) INFORMATION FOR SEQ ID :905:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 225 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25	GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTTAGAGA AACCAACGGT	50
	AAAAAAAAAAA ATAATAATTAA ATACCGTTGG TTTCTACATA CACTCTCAAT	100
	ATTTGCACGA GTAAAGCGTA GCAAGTTAA CACAACTTAT GTAAACTTGG	150
30	AAAATTTCC GAAATTTAT TGACTTTCT CGGTCTCTCC TATCTTTATA	200
	TACACATCTC TCATGCACAC ACGCG	225

35 (2) INFORMATION FOR SEQ ID :906:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 161 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

458

(xi) SEQUENCE DESCRIPTION: SEQ ID :906:

	GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA	50
5.	ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA	100
	TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG	150
10	TCCACTGTAG C	161

(2) INFORMATION FOR SEQ ID :907:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 204 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :907:	
	AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTAAAAT	50
25	ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT	100
	TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT	150
30	TATATATGCG CACACACACA CACACACGAC ACCGACGACAC ACACACACAC	200
	TCTA	204

(2) INFORMATION FOR SEQ ID :908:

35		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 316 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

459

(xi) SEQUENCE DESCRIPTION: SEQ ID :908:

	AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA	50
5	AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC	100
	TGCCGTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC	150
10	ATATGGGCAG GACAGAGCTC TTCAACCCCTG GCTAACAAAGC CTGAAGAAGA	200
	CCCTGTGAGG CCGCAGCAGC CATGGAACT TCCCAAAGGA CAGAAATCCA	250
	CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCCTT CCACCATATC	300
15	CAAATGTGTG TGTGTT	316

(2) INFORMATION FOR SEQ ID :909:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 307 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :909:

	CTAGAACAT AGAAAATAAA CTTCAGTGGG AATCTCTGCT TCCCGCGTGA	50
30	GGTGTAAAT TCTTGGCATT TTTGTATTTT AAAGATGTAG CAACTTGTAA	100
	CAAGTTAGAG GAGATGGCAG GGTCAAAATT TTAGAAACTG GATCCCACCA	150
35	CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA	200
	TGTGCCAATA GAATTATACG GTGTGAAC TG CATATCTCAG TATCTCCACG	250
	GGAAAAAAACT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTAA	300
40	GCTATTT	307

460

(2) INFORMATION FOR SEQ ID :910:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTGCTC AATCAAACGC	50
15 AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT	100
TAAACCGAAT CCCCACAAATC TCAAACCTCAA CCAGGCCAAA GGGAACACAG	150
20 TGACACAAACA ACAGGGTTCC AA	172

20

(2) INFORMATION FOR SEQ ID :911:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA	50
35 CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG	100
AGAGATAGAG AGAGATACAC ATACACACAT TCATCAACGA GAGAGAAAGAG	150
AGGAAAGAGA GAGAGAGCGA GCACAGACAG AGATAGAGCA CACAGAGAGA	200
40 TCGCGCAGAT CTATACAGAG CGATATTACAC CACATTGTAT ATGGAAAGCG	250

461

CATCT

255

(2) INFORMATION FOR SEQ ID :912:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :912:

15	CAAGCGAATG GTAATTACAT GGTCGGATGA GGTCCCTCACT CTCAGGGGAG	50
	GGAGGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACACTGTTT	100
	GAAGGCATCTA ACGAAGGGCA ACAGTTTTG GCAACCCAAT TCACAGTTT	150
20	GCAATTACCA AGAGATTCT TTGAAAGAAA ATAGGAAGGC AAAGAA	196

(2) INFORMATION FOR SEQ ID :913:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :913:

35	ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA	50
	GCGATTTTAC AGTAGAGTGA ACGAAACTNG AGAAGGAAAA CATCCAAGAG	100
	GCATCTGTTT GACCGCAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA	150
40	TCCCACTAGG GCCACGAGAA ACAAAGCAA TTAAACATT ATCCACTACA	200

462

CGA

203

(2) INFORMATION FOR SEQ ID :914:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15	CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA	50
	GGGTCTCTTT TTCCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT	100
	AGCCTGGCTC TGCCCCGCAG AACGGTCTGT GTGCTGTTG AAAATAAAC	150
20	TTAGTGTCA AAACAAAATG AAACAAAAAA AAAATGATAA AAAATCGGA	200
	TTTCCGGTTA ACACTGTGAC TTCAATTGAA ACACCTTTTG GTAGTATCTG	250
25	GAGGTGGACA TT	262

(2) INFORMATION FOR SEQ ID :915:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :915:

40	TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT	50
	ACACGGAGTC TGTATTTGC ATCCTAGAAT GATTAACCAAG AAACAAAGAA	100

463

ACGAAAAAGG TAAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT	150
AAACAATGAA ATAATTGAA AAAAAAGGCA GGGCAGGCAA A	191

5 (2) INFORMATION FOR SEQ ID :916:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGTTT	50
TCCAGGAGTT GTCCTTGTT GTTTGTCGTG AAGAATTATA CTTTGTGTG	100
GTGTGGTTG TCCCATGTGT ATGCGTAGTGTAG TGTGACAGTA TATGACCCCC	150
AGTGTGTGCA TATGTTGTC TGTTGTCCTC TGAGTGATAT CCACCTCTCT	200
CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG	250
TG	252

30 (2) INFORMATION FOR SEQ ID :917:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :917:

TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA	50
--	----

464

	GTAGGGAAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT	100
	TCCTGAAGGT CATGCGATCC TTTACCCCTCA GAAACTTCA GGCTGAAATC	150
5	ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCAGTT	200
	CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC	247

(2) INFORMATION FOR SEQ ID :918:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :918:

20

	ATTTGGATTC AATTGCCTGT TGCACCTTTA CATTAAAGTGT TGCTTAAATA	50
	AACAAAAATA GAGCATAAAAT TCAATATTCT ACTGTCTAAA CATTAAAG	100
25	CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTT	150
	TGACACCTCT TGTTTAAGT TTCCTGTATG ATAAAGTTCT T	191

25

(2) INFORMATION FOR SEQ ID :919:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :919:

40

	CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAGAAAG AAAAAAAGAA	50
--	---	----

465

	ACAAACCTCCT CATTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG	100
	ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT	150
5	CGAACAAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCC	200
	AACCC	205

(2) INFORMATION FOR SEQ ID :920:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :920:

20

	GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTCCCTC TCCAACGACT	50
	CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA	100
25	CATCTCCTAT CGTTAGTTGA ATAAATTACAC ACACCGCGTT TAAGAGATGA	150
	AACCACGACT TCGTCAAGCC ACATTGATT GCCATAAGAT TCCAAAGAAT	200
	TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA	250
30	AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG	300
	CTCTAAGCTA CAGGTTGATC ATA	323

30

35

(2) INFORMATION FOR SEQ ID :921:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

466

(xi) SEQUENCE DESCRIPTION: SEQ ID :921:

	AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAAGTCTGCA	50
5	GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG	100
	ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG	150
10	GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCAGGCGG GGATCAAAAC	200
	TATAGAAACA ACAAGTTAGA GTACAGACGT	230

(2) INFORMATION FOR SEQ ID :922:

- | | |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 239 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 20 | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :922:

25	TATTTTCCT GATGTTCTCC CTTCCCTCCAG TCCCCGACCT CCCACAGGCC	50
	CCAGTGTGTG TTGTTCCCGT TCCTCGTGTG CGTGAGTTCT CATTGTTCA	100
30	TGCCCATTCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCCTCGCTC	150
	TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC	200
	TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTTGTAA	239

- | | |
|----|----------------------------------|
| 35 | (2) INFORMATION FOR SEQ ID :923: |
| | (i) SEQUENCE CHARACTERISTICS: |

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 178 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5	GTCAGTTCAG TTGTGAACAA AGCCCCTTGT GTACGTTTT AAATTTAGT	50
	TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT	100
	TTATGGATGA GAAAACAACA GAGAGTTGA TTGGCCCCAC CTTCAAATCC	150
10	TGAAACCCGT CCACTCAATA AATTTTTG	178

(2) INFORMATION FOR SEQ ID :924:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25	CAGCTGGTCC CCCACTAAAAA GAAGGGCAG ACCACCACTA GCCAAAAGAG	50
	ATAGCAAGAC TAACATCTGG AAGAACGAG AGGAACGCC ACTGATTCCC	100
	AAAAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTAT	150
30	TCTTGCTTCT TGTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA	200
	GCAATCTCAT GGTTCTTGGG CATGTCCAA GCAGAGTAA TGGTAATTCA	250
35	GTAATCAGAG AGAAAGATAC CAAGGAATGC TTTTCTGGC CTATTCATTT	300
	ATTTTTGGGG GATGAATTAA CAGTA	325

(2) INFORMATION FOR SEQ ID :925:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 base pairs

468

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :925:

	ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG	50
10	AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT	100
	CCGGTTTTCT TTGTTTTTC TCTTTATTCA TCCCTTCTCA AAGATGGGAT	150
15	ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG	200
	AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG	250
	TTCCAGTCCT G	261

20

(2) INFORMATION FOR SEQ ID :926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :926:

	GTCAGCCTGG CCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC	50
35	AACTGGGTTTC AAATCCTGGC TCTGTACAT ACTAGCTGTG TGACCTTGGC	100
	CAAGTTTCTT AACCTCTCTG TGTGTATACT CCTTATCTGA AAATGGGGAT	150
	AACCAACCAA GAGAGCTGAG AGA	173

40

(2) INFORMATION FOR SEQ ID :927:

469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :927:

10

AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC	50
CTCGCTTGCT TTGTAGTTT CCCGCACCAG CCCGCTGCC TGCGCCATCC	100
TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC	150
CTTNGATTTT TCTGCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCGAC	200
TCAGATCATT ACTACTGAAC TCG	223

20

(2) INFORMATION FOR SEQ ID :928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :928:

GTTATAATTAA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT	50
ATTTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTT AAGATAAAAA	100
CCACAGATTAA AGTGAAGACA CCCACAACCT TAATGACTCT ACGACTCTCG	150
GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT	200
CATAACTTGC AT	212

40

470

(2) INFORMATION FOR SEQ ID :929:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :929:

	TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAATT	50
15	ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCCTAGTTT GATATATGAT	100
	TACTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTGTG	150
20	TATAATGTTA TGTTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG	200
	ACATAACTTG AGTTTGTGTTG CTTGGTATTT ATT	233

(2) INFORMATION FOR SEQ ID :930:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :930:

35	AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA	50
	GATCAGATGG CATCCAGAAG ATAGTTAGA TTTCAGCACA TTCATGGTTC	100
	AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTAC AATCATCATA	150
40	GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC	200

471

TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG

235

(2) INFORMATION FOR SEQ ID :931:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :931:

15	CTATCTAGAA TTACTTATTTCAC TTGAAAT GTATGGTTTC AGGAAAATTT	50
	TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGGATAATGGCAT	100
	CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTTGGGT GAATGCTTAA	150
20	AAACAAAAAA AAAATTTACA TATGCATTTT ATGGATAACAC ACACACACAC	200
	ACACACACAC ACAAAAAACA C	221

25 (2) INFORMATION FOR SEQ ID :932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :932:

	TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG	50
	CGTCATGTCT TGTGCTACTA CACCGTGTAA ATCCCAGCTA CTCAGGAGGC	100
40	TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA	150

472

TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG	200
GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA	250
ACGGAGCAGG TCAAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT	300
GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA	333

(2) INFORMATION FOR SEQ ID :933:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :933:

20

30

(2) INFORMATION FOR SEQ ID :934:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

473

(xi) SEQUENCE DESCRIPTION: SEQ ID :934:

	AATCTTGTAT TATGTTAATA TTAAAATCTA ATAATAAGAT ACTGTAGAAG	50
5	TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG	100
	TAATAGAATT GAACAATTAA CTATAAAATA TTATATCATA ATAAACTGTT	150
10	GTTTATCCC AAGGGTAGAG GGACTCTAAG TAAAACTGTA ACAGAACCAA	200
	AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTAA CTTGGGAACT	250
	TTAAATAAGT AAATCT	266

15 (2) INFORMATION FOR SEQ ID :935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :935:

	GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAACT	50
30	ACTAATAACT CATTAATAAA ATTAATAATA TTAAATGATC TGTGTGTTCC	100
	ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAAATA	150
	TTACTCTAAC ACCAATAACA ACACGTAA	178

35 (2) INFORMATION FOR SEQ ID :936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

474

(xi) SEQUENCE DESCRIPTION: SEQ ID :936:

	ACTCAGCTCC GTGCGACCCA CATGGCCCCA GGCGGGGGGA CACCAAGAGC	50
5	TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCT ACAGCAACTT	100
	TCCCAGCCAA TGCCACGATG GAGATGACAA CCCCAGATCT GGGGANACAG	150
10	AAACCACCTCA GAACGGCACA GGGTAACTGG CCCCAAACGC TGAAAGTTAG	200
	ACTTCACCCG AATTACATTT ACCA	224

(2) INFORMATION FOR SEQ ID :937:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :937:

25	ATTTTTTTTC CCAAGAACATCC CCAACTCAAT AAAACCGTGA AACAAATTGCT	50
	GGGGATGGGT AGAGAAAACC CATTATAGT ACTTTTCTGC CTTCTTGCG	100
30	TTTTCGGCTT TGGCATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAAA	150
	AAAACAAACA CAAAAACATT TCAAAAGAGA AAGGAAAAAA CTTTTTCCAA	200
	CCAAAACCTCC TAAAAAACCC AAAAACAGAA CAACCAATTA AACCCGACCC	250
35	GACACAACTA CCAATGACTG	270

(2) INFORMATION FOR SEQ ID :938:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 215 base pairs
 - (B) TYPE: nucleic acid

475

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :938:

	AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG	50
10	AACTTGGAAC TGTCA TGAGG TCACTGGTC AGAACCCAAC AGAAGCTGAA	100
	TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA	150
	CTTCCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA	200
15	CTAGAACTAA AGTCA	215

(2) INFORMATION FOR SEQ ID :939:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 303 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :939:

30	TGTCGTCC TT AATATTTCTN AGCCTTTGT CATAAGAGTG GTGGTTGGA	50
	CCTCAAAGCC TCCATCTAAT TTTTTTGTC TATGTTCTA TATCTCTCTC	100
	TTTTACGCTT CTTTCCCGGA CCGTCCCCTC CCTCTACAAT TATATTTACT	150
35	ACCTTCATGA TTGCTTTTA TTATTTCTT CACTCATCAT TATTGTTCAT	200
	TTTTTAATTA ACAATTTTT TCATTATTCT TTTCTTAAT TTGTAACCCG	250
40	TTTCTAATTT TCTCAATTAT TGCGCTTCT CAACCCCCCT CCTTCCTCAT	300
	TAC	303

476

(2) INFORMATION FOR SEQ ID :940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :940:

	ACACTATTTT CAAAAATCCA AATAAAAGTG CAGTTTCAGA CTTTTTAAAA	50
15	AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG	100
	CGTTTGCATG CAACACTGCA TATTTTTCT AATCAGATTA ATATGAGTTT	150
	TAATGTTAG CATGAACCTAC AGCTAAGGAT AAAAATTAA AAGTAGCTTT	200
20	CATAGTCTAG ATTCCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT	250
	TGCTTTGCTT TGTGGAGACT TGCGCGTATT TTCTTTGCT TGTTTGTAA	300
25	TCGCCAGGCA GCGCTGTTCG AACTGTGAGA	330

(2) INFORMATION FOR SEQ ID :941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :941:

	TTTATTTCAAG ATAATTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT	50
40	TTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAAATGCAT	100

477

TTTGCT

107

(2) INFORMATION FOR SEQ ID :942:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :942:

15	CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTG GTGTGTATGT	50
	GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGGAG ATTTGGTTAT	100
	TTCGGCGTTA CACCTCCGGT GTTCTC	126

20

(2) INFORMATION FOR SEQ ID :943:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :943:

35	ACTGAACAGC CGCTGGTTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA	50
	AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA	100
	GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA	150
	AGCTC	155

40

(2) INFORMATION FOR SEQ ID :944:

478

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10	CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT	50
	TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG	100
15	GGGGGGGGTT TGGAAGCAAA CACATTGGG GTTTTAACC AATTGTTAGG	150
	TTCTTTTAT TTAGGGTTGT GCAGGGAACG GTTGGGAGGT TTCTTTAGGT	200
	GGGATGGGG GACTGGGTGT TGGTTTTGG GGGGTTTTG GGACGGGTTT	250
20	TATTTTGTCCTTAACTTGG TTTGTTGGGC AGGTGGG	287

(2) INFORMATION FOR SEQ ID :945:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :945:

35	ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCC AAATCTCTTG	50
	TCCAATTATA ATCCCCAGCA TTGGAGGAGG GGCCCGGTGG GAGGTGATTG	100
	GATCATGGGC ATGGACTTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT	149

40

(2) INFORMATION FOR SEQ ID :946:

480

TTTAGCCACT TAAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC	250
CAAGTTGTAT ATTT	264

5 (2) INFORMATION FOR SEQ ID :948:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCCAGAACAT GACTATCAGC GGTGTTTGA	50
GCCAGGTTGA TTGAGCACTG GGCTCCAAT TATTGTTAAT GAGAAACGGC	100
20 CCAACTTGGA CCATGACTTT CCCATTGCA GGTCTTAGAA TAATTTTT	149

(2) INFORMATION FOR SEQ ID :949:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :949:

35 CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCAG	50
GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA	100
40 GGCCTCCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG	150
TTCTAGTCCC CTTTTAGAT CCTAGGGAC TGGAGATTTG GCACCTTCCC	200

481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT

242

(2) INFORMATION FOR SEQ ID :950:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :950:

15	ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG	50
	CACTGACAGA TTTACAGACA GGAAACAAA GCCTTACTTA CCAGGAATCC	100
	AAAGTTTATA CATGAAAATT TAAAAAGGGA GTCTATGCAA AGCGGAGTTC	150
20	AGG	153

(2) INFORMATION FOR SEQ ID :951:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :951:

35	TGCGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG	50
	TTGTTCTAA GGCGAGCTCA GGGAGGATAC AGAAAACCTCT CCTGTGGTGC	100
	TATGAAATGT GGCGTAAAAA GCATTCTG	128

40

(2) INFORMATION FOR SEQ ID :952:

482

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :952:

10 GTTGGAAATT TCCC CAAAT CACCTACCGA TTACCCCTTGA TTTCCCTTTG 50
TTTCAGTTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC 100
15 ATATAAAAAT AAAGTGTACC CAAATATTGT AATGTATATT GCTGCTCTTC 150
TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC 200
AATTGATACA AAT 213
20

(2) INFORMATION FOR SEQ ID :953:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :953:

35 GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTC 50
TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100
40 TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAGACTAC 150
CACAAATCCTG GATAACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT 200
GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT 236

483

(2) INFORMATION FOR SEQ ID :954:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :954:

	GCAGCAGTTT CTTTGAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTC	50
15	TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT	100
	TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAAC	150
	CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATTT	200
20	GCCACTGCAG AAAGTGT	217

(2) INFORMATION FOR SEQ ID :955:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :955:

35	AGCAGCGACC GCGCTCACTG GCTTTTGTT TCTGCTTGGG CCTTTCTGT	50
	TCAGTCCATG CTTGAAC_TAC TCCACCCCT TAAATCCAAC GTAAAAACCA	100
	GTCTTTCTG TGCTTGTCT CTGTGCGTTA ATGCTTTTC TTATGCTTGC	150
40	TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG	200

484

TGAAACCATT TTAGATACTC TACTTCTTA CTGTGTTACG TGGCATTAA	250
TGCTTG	256

5 (2) INFORMATION FOR SEQ ID :956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTTT TTCCCTGTTAT TTTTCTACCA TTTATTCTC	50
ATTCATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTATT	100
20 AATTTTTAAA AATAACATTA AAAAATTTTT TAAAATGTGA ATATACCACA	150
ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA	194

25 (2) INFORMATION FOR SEQ ID :957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
ATAAACCTAAA AAAACATGTT TTCTCCACAC TAATTTAGG GTGAATTCCCT	100
40 CATTTCGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCG TGTGTGTGAG	150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA

196

(2) INFORMATION FOR SEQ ID :958:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15 GCGCTCAGCT GGAACCTCCG ATCTATTTC TCTTGGTCTC ATACTCAGTT 50
TTTTTATGTA GTCACCTTAGT AAAATAAACCC TAAAAAAA CATTGATTTC 100
TTCTG 105

20

(2) INFORMATION FOR SEQ ID :959:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :959:

35 GACAGCGACC GACACTCAAT GGAATCCCCA TTCCATGGAA ATGGAAAATA 50
GCTCTATTAA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA 100
TAATTCAATTA ACACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACCGAT 150
TATCATGATC TGCATTCTTG ACAAGTATAAC TATGGCGAGA TAAATCAAAC 200
40 TCAGACGATG ATAAGCAAAC TCAAAATGA AAATGATGAT GCCAACTAAC 250

486

CTTTGTTAA A

261

(2) INFORMATION FOR SEQ ID :960:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 188 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15	CACAGTTTG TTGACTAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA	50
	TCGTTTCTTC TTTAGAGGAG TAGGTTTAA CCATGTTAA TTTCCAAGAA	100
	TAAATTATT TATCACCTCT ACACAGCGCA GACCATTCA GGAAAATAAA	150
20	TAATTTTCGA TTCAAGTACT ATACAAACTT AACGATGG	188

(2) INFORMATION FOR SEQ ID :961:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35	ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC	50
	TTCACCCAGC AATACTGCCT ATGCAACCT GGAGCTTTTC AATCCACAGA	100
	CACACGCTAT GCACTGCTCT TCGCCATCAT AACGCTAAC ACCAATTCT	150
40	ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C	191

487

(2) INFORMATION FOR SEQ ID :962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT	50
ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA	100
TCAATGAATA TACAAC TGAC TGGATTTAA ATATACACAA ACCAGTATAC	150
CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAAT T	191

20

(2) INFORMATION FOR SEQ ID :963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCAGC AGGAACAGCA GCCCAATGCC	50
TCCTAGCACT CAAGATCCAC CATA GTCCAA GCAACTGCAG TTACACTTGA	100
GTACAAATAC GCTCCGACA GCCTCATGCA GCGACACCCCT AAAGGACACC	150
CGAACACCAT CAATAACCGA ATAGACTA	178

40

(2) INFORMATION FOR SEQ ID :964:

488

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :964:

10

ACTTTCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG	50
GGGATCCTTT TGACTGCCAG ACGCGGAAAG GAAAGAATGA ATTAAAGAA	100
TATCCTTTTA AACACACACC TCGACACAAT TTTCACACTCT GCTAAGGGAT	150
CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC	199

(2) INFORMATION FOR SEQ ID :965:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :965:

30

ATGGACCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGTATTT	50
GGCACATCTG CCAAAAGCTA CAAACAAACCC CTAATAATTA CACACTACAG	100
ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT	150
CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTCTCC TCGCCTTAA	200
ACCTGCAGGT TGGGGCT	217

40

(2) INFORMATION FOR SEQ ID :966:

489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :966:

10

ATTTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTCC 50
AATTAAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCAATTA TCACTAGGAT 100
15 CAAGAAAAAG CAAATGGTTT AAGTTTTAC ATAGGAAATC TAAGAACTAC 150
TCATCAATAA AACGCAACAC TATCA 175

(2) INFORMATION FOR SEQ ID :967:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 92 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :967:

30

AGGGGTTCAAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG 50
GGGGACAAGG AAAACCTGGC GCCCCCCCACC GCGAAAAACA CA 92

35

(2) INFORMATION FOR SEQ ID :968:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

490

(xi) SEQUENCE DESCRIPTION: SEQ ID :968:

	GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA	50
5	TATTGTCAG CAGGAAAAGT AAAACTTCAG AAAAATTCCC TAAAGATCCT	100
	ATTCAATAAA CAATTTAGA TTTAAGGAAC CACTTACGCA AAACTCGAAC	150
10	AAATAACCGA AAACCTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA	200
	CTACTAAC	208

(2) INFORMATION FOR SEQ ID :969:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 256 base pairs
	(B) TYPE: nucleic acid
20	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :969:

25	AGTGGTTGGT GTTTACTGGA ATCTTGTMTT TTTTTTTTCG GTTTTTTGAA	50
	CTACTCGGGG GGTTTCCTT TTTTACAGGA ACTAAATCAA CAAACTTTTT	100
30	CGATTCCCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC	150
	TTCATTTAAA ACTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC	200
	CACCAAGGAT TTACTCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT	250
35	TTAAGA	256

(2) INFORMATION FOR SEQ ID :970:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 240 base pairs
	(B) TYPE: nucleic acid

491

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :970:

20	AATCTATTTT CCTGGTCTC ATACTAAGTT TTTATGTAG TCACCTAGTA	50
10	AATAACCTAA CCGCTTGTT TTTCCACAC TAATACTAGG GCGAATTCT	100
	CATTTTATTT TTAAGATCAT GGGCGAGGG AGATGATCGC GAGCACGAGG	150
	ACCTAAGACA TCAGATGAAA ACAATGCCT CTATTCTTC AAGTATAATA	200
15	AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA	240

(2) INFORMATION FOR SEQ ID :971:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :971:

30	ATCTATTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
	ATAACCTAAT CCGCTTGTTT TCTCCACACT AATCCGAGGG TGAATTCTA	100
	ATCTAGCTTT TCAGATCATG GGACGAGGG AATGACCGCG TGCGCGAGGC	150
35	CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT	184

(2) INFORMATION FOR SEQ ID :972:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid

492

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :972:

	GTGTTCTCTA AGGTGATACC TTTTAATTAA GAAAGACTAA ATAATTAA	50
10	TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTTAATTCA CTACTTGTAA	100
	CATAATCCAG TGAAAACCTCT ACTTGTTGAA ATTATGACAT AAAGATCTTG	150
	CAGCTTTATT TGAGTATTG TTCTTTGTG TAGTTTCCAT CTTTTAAAAT	200
15	ATTTAAAATA TTTTCAAGGA TAAAAGTATT ATCT	234

(2) INFORMATION FOR SEQ ID :973:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 197 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :973:

30	TTTTCATCTA AAGGAGAGAG GCAGGGCTCAG CTCCTGAAGG TCGCAGAGCC	50
	TCAGTAGTCC TCCTGAGTGC GTCTAAGTAA CTACCATCAA AAAACAAACA	100
	AAAAAAACAT CACAAAACGT AACTGCCGCC ATCACCACTA CACCAAGTAT	150
35	GTGATTGAAT TATTCAATGA TCTGTTTCG CGGTAGTGAC CAACANC	197

(2) INFORMATION FOR SEQ ID :974:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 244 base pairs
	(B) TYPE: nucleic acid

493

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

	AGCAGGAGAT TTTTTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG	50
10	ATGGAAAAAC AGGATCAAAG GAGCACACATA TCCAGTGACT TAAAAAAAATA	100
	ATCACACGTG GCAAGAACGTT TTCTAAAGTA AACTGTATGT GGGGAGAAC	150
	ATACAGAAAA AACGAAATA CATAACCCCC CAGGTTGAA AGAAAATAAT	200
15	TTTGAGTTGT ATCAATCTAT CGATATCAA GAATGAATGA CCGC	244

(2) INFORMATION FOR SEQ ID :975:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 330 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :975:

30	TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG	50
	AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG	100
	AGACCCATTA GAGATTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC	150
35	ACCTTACTAT ACACATAATA TAGAATCTGA GGACTACGTT AACTGATACA	200
	TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT	250
40	TAGCTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA	300
	ATGTGCAATG AAGGGTTTCG TGTAATATTG	330

494

(2) INFORMATION FOR SEQ ID :976:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :976:

	TGGTGAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT	50
15	TCTTAGAAC GTAGAAAGAC TGCAGGGGAA AATAATTAAA GCAGCTTTAT	100
	TCCTTACGGC ATTCACTCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT	150.
	AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTTATAT GAATNACTTA	200

20

(2) INFORMATION FOR SEQ ID :977:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :977:

	AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT	50
35	ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT	100
	AATGATGTTA TGAAACGAGC TTTGCT 3 GCTCTTGATT GGAGCTTCCG	150
	GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAC. 3 AACTGTGTTT	200
40	AATACTCTGA ATTTTAATTA GAAAAAAATA CAATAGCAGC AAGGCCCTGG	250

495

TTTCTAAGCT GCATACTTTT ACTAACCGGG GACATGAGCA AATGCC

296

(2) INFORMATION FOR SEQ ID :978:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :978:

15	GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG	50
	ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT	100
	AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGAAAGC CGGGGGAGGA	150
20	CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCAGAATC	200
	CAGCCACTAC TGATAATTCA CAACGGTA	228

25 (2) INFORMATION FOR SEQ ID :979:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :979:

	CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCCTACG GGAGGGTTAT	50
	CCCCCTGACG CTAGGCCATG ACACAACCAA ACTTCAATAC ACCAGGACTA	100
40	AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA	150

496

CCAGGGAAAAA CCAGAACCTG A

171

(2) INFORMATION FOR SEQ ID :980:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :980:

15 TGATTCCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGGAGC 50
 CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCTAC
 CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTTT CACACCAATG 150
20 ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATTA 200
 CTGCAGTGGAAATAACTGC ACTCTCAGGA CACAGCACTG T 241

25 (2) INFORMATION FOR SEQ ID :981:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :981:

40 TCACTGCAAT CACGGTAGCT TCGCCCATTG CCTCTTCAAC CAGGCACATA 50
 CATCGAGAAG TTGAACCTGC ACTTTATTC ACAGTGAACA GACTTACCCC 100
 GACAACAAACA CCTCCCCAGT GGGACAAACC TACCCCACCT CCCCCACACTC 150

497

TACTCCCAGC TAAACGTTCCC TATAATCATC ATGACCCATT AAACATTTGC	200
AAAACCACAC TTCAACCCAC AGGAAGA	227

5 (2) INFORMATION FOR SEQ ID :982:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - 10 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG	50
ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT	100
20 CCGCGAACTC ATGACTGACC CCTTCTAAGT AAGAATCCCA CCCAGGCAAA	150
CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC	200
25 AAAAG	205

(2) INFORMATION FOR SEQ ID :983:

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTAA AAAATGATCT	50
40 TACCTGTACC AGAAAAGCAA ATTAAAGGA AACAAAATAA GAACCATAAGT	100

498

CCCAAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA 150

CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC 200

5 CCCT 204

(2) INFORMATION FOR SEQ ID :984:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :984:

20 ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTTG CATTCTTGTT 50
 TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTT AAAATCCACT 100
 AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTGCT TTTTTTTTC 150
 25 TTTCTCCCCC CTCCCCAG 168

(2) INFORMATION FOR SEQ ID :985:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :95

40 CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCAG AGAAGCATGG 50
 GCTGGGCCTG GGCAACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT 100

499

	TTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCCA TCTCCAGGCG	150
	CTGGGAGGGG GGCCCTCACCC CCGTCACGCC TCGCTCCCTC CTGGCCCTCT	200
5	GGTCCAGCCC CTTACGCCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT	250
	CCTGATGTAT TTTTTTTTCC TCCAACTCAA AAGGCAAAAA TAATCCTATT	300
	TTTATTATCT TGCTACAACT GCAACTTTCT GCCCTATAAA TTTACATTCC	350

10

(2) INFORMATION FOR SEQ ID :986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :986:

	AGCGACCGCC ACTCACTGTG AGTTCCACTT AATTCAAGGTG AGCCGCTCTT	50
25	CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTTGAAGGT	100
	TCAACAATGC TCTGCAAATC TTTTTAAGAC CCGTTACTTC AACAACTCCC	150
	AATAACCTTCC TCCTCAACGG AACAACTTAA CCGTTACCTT TTAAACCCGA	200
30	CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAAATTCTA CAAAGGACCA	250
	AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAAA	289

35

(2) INFORMATION FOR SEQ ID :987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- 40 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

500

(xi) SEQUENCE DESCRIPTION: SEQ ID :987:

5 CACAATCATA GCATTTATTA CACGATTAC ATCTGATCCT CACGCAATT 50
TCTTCCTCAC CAATAAAGAA CTAATAGGAC AGCATATTAG AAGAACATA 100
CATTCTTTA TTCTTGCATC GCTATAAAGA AGTA 134

10 (2) INFORMATION FOR SEQ ID :988:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear,

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :988:

TTCTGAAATG AAGGTTTCGT CTTTAGCTAT TGACTGTAGG ATTTGTAATT 50
CAAATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA 100
25 ATTCCCTACAG AACACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG 150
GTGGCTCTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT 200
TCATAATTAA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG 250
30 ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC 287

(2) INFORMATION FOR SEQ ID :989:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID :989:

AGCAACCAAC ACTCACTGGA ATCCCGCAAT CAAGAGCTAA AAGGACTTCT 50
5 TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCCTG 100
AATGACTCTC ACTGGCACTT TTAAACACAG CAAGCCCAAC ATATTTCTC 150
CTTTTCATAA AGAACCTAT ACACCAT 177
10 (2) INFORMATION FOR SEQ ID :990:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :990:
TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA 50

25 TAAACTAACCC ACCAACCAAA GGAGGCACAA TCCAACGAAA 100
CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAC 150
CAAAAGTC 158
30 (2) INFORMATION FOR SEQ ID :991:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :991:

502

	TAATCCCTTT TAAGCAGAGA TACACATTCA CAGAGAGAGA ATGTTTAAA	50
	AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTAAT TCATTTGAT	100
5	TACACAAAAA TAAGGCAAAC TAAATGATTC AGAACAAATTC AATTTAACTG	150
	AAGCCTTCTA GAAAAATACT CAACAGGCTT CAACAAAAAG ACTTAGCGCA	200
	CATAAAACAA TCACGAAGAT CACAATTCA GCACAAATAT CTGAAGGAAT	250
10	ACACGCAAAA CATCATA	267

(2) INFORMATION FOR SEQ ID :992:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 199 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20.

(xi) SEQUENCE DESCRIPTION: SEQ ID :992:

25	AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACAGTGA	50
	TTGTCAAATT CCACCTTGCA TGGAAGACAG CACAGAACCC TGCTCTGGCT	100
	CAGCTGGAGA GCTCCGGCCA GCACGGCAC CAGCAGCATG ATCAGTGTGA	150
30	TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA	199

(2) INFORMATION FOR SEQ ID :993:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 198 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

503

(xi) SEQUENCE DESCRIPTION: SEQ ID :993:

	TTTAAGGTGC TAAACTTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG	50
5	ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCCTGCGAGG	100
	AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT	150
10	AGCAGATCTC AGGCGTAACC ATTCGCTAAC TGTAUTGAAG ATGCGTCC	198

(2) INFORMATION FOR SEQ ID :994:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 183 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :994:

	GCTATCTGCG GGGCCATTG TAGGATGGGT GAGTCAGATG ATTCCATTCT	50
25	CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGACTGGAGA	100
	GAATAACAGA CGTGGAAATAT TTGTCACTAA TAAATAACGA AACCTAAAAA	150
	AAAAAAAAAAA ACAACAAACC CCAACAAACT CAA	183

30 (2) INFORMATION FOR SEQ ID :995:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 35 | (A) LENGTH: 199 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :995:

504

	ACCTCTGCAT TAAACACTCCA GCACCTTGG TTAGCCAATT TGGCCTTATT	50
	TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAGG AATGTTTCG	100
5	GGTTACCCCA CTGTCCCCAA CTTCGAATAT GCTCACTGCC TGGAAAATGT	150
	TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA	199

(2) INFORMATION FOR SEQ ID :996:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :996:

20

	GGTCTTGGCT GGTGGTTAT GGCCCGGGCC TTCTTTCTAC GGGGGCCAGG	50
	GTCCAATTTC CCACCTGGGG TTTAAAAGTT AAGGAGGACC AGCCTGGAA	100
25	CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTA	150
	ACGGGACACC ATATGGAGAT TTTATGC	177

(2) INFORMATION FOR SEQ ID :997:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :997:

40

	GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAAC AACATTCA	50
--	---	----

505

	GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTC	100
	ACTGAATAAT TCCTCTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC	150
5	GTAGAAAGTT GCTTGAAATT CTTTCCTAA AAAAATTAA TTTTTCTATC	200
	TCAAAATGAC CGTATGCAAA CGAACATTA	229

(2) INFORMATION FOR SEQ ID :998:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :998:

20

	TTGCAGTGTT TATGCCGCC TTCTTCACG GGCAGGTTCA ATTCACGG	50
	TTTAAAAGTA AGAGACAGGC TGAACCCCTTC GTGGAGCCAT TTCATTACAG	100
25	GTCCCTTAAT TTAAGGAACA AGTTGATTAA TGCTACCTTT TTGCACGGTT	150
	TAGGGTACCG CGGCCGTTAA ACATGTGTTTC ACTGGGCCAG GCGGTGCCCTC	200
	TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT	233

30

(2) INFORMATION FOR SEQ ID :999:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :999:

506

TCAAAAACTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTGGCTT	50
CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA	100
5 TGTGGCTGGT GGGCCATGGG TTGGACAAGC TTGATGTAAA TAAAACCACC	150
AGTGGAAAGA GTTTGTTGTG AGTTACATTC AAATACAACA GGAGTAATAC	200
TATCATGATA TTAGTT	216

10

(2) INFORMATION FOR SEQ ID :1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1000:

GACAAGACCT AGAACGAAACA ATGCCAGTA GAAACAAACA CACCTACTGC	50
25 CTGGATCTTA GTTTTAATT ATATTCCCCA ATAAAGAGAC CCAGGGCTCC	100
TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA	150
CCTAGAAATAT CTAATACTGC CAAAAATTAA GAAAGTGTTC TAAAAAAAAT.	200
30 CCCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCCATCT GAAGGAGTTC	250
CCAATGGCCA AAGATCAAAT AATTTTCAA	280

35

(2) INFORMATION FOR SEQ ID :1001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- 40 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

507

(xi) SEQUENCE DESCRIPTION: SEQ ID :1001:

	TGCATGATAG GAGCGTCCTT TGTTCTCATG AGGTGACTCT TGGTGGGCTC	50
5	CTTATTTGGG GACTGGTCAC CAAAAATAACC TAACTATGGT TGGAAAGCTTA	100
	GTGCTTTCAG CCCCCATTCCC CATCCTCTGG AAAGGGGAGC AGAGCTGGAG	150
10	CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAAATCCT TGAAAGACAG	200
	GACATGGAGA GGCTGCTGGG TTGGCGAACCA CAGCCATGTG CCGGGAGGAT	250
	GGTGCACCCC AACTCCACAA GGACCCCTCC AGACCTCACCC TGTGTATCTC	300
15	TTCATCTGGC TGTTCATTTG TATC	324

(2) INFORMATION FOR SEQ ID :1002:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1002:

30	ATTCACATTG ATAAGTCCTC ACAAAACCCAC TTTTCCTCTT GCCTGAGTGC	50
	CTCACATACC CTACTGCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCTCC	100
	CCCAACGAAA CACCAGGCAC ACACCTGCC CCAGTCTTGC CTGCACTCTC	150
35	CTTTCCCTCCC GCAGAGAGGC ATTCCCTTCT CCTCCTCTCA TCCTACACAC	200
	ACTATAAGAG ACAACTGAAA TCTTGCCTCC TCCAGCAAGC TTCTTAATTG	250
40	ATTT	254

(2) INFORMATION FOR SEQ ID :1003:

508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1003:

10

AAGGTTGCCG	TGCCCCATCCT	CTCGCCCTTC	GGAATTTACC	CCTGGCCGCT	50	
CAGGGTCTCG CTTCTAGAAC					100	
15	TTGCCTTTAT	ATTTAACAGG	CCCGCCGAGG	AGGGGCTCCC	GCTGGTGCCC	150
ACATAACTCT ATTAGACCAT					200	
CTGAGGCAC					250	
20	TTGAGACTA	TACTG				265

(2) INFORMATION FOR SEQ ID :1004:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1004:

35

AAATATGCC	TGAGGATTAT	CTGATGTCGA	TGGTGTGGAA	AAGAACCTCA	50
GCAGGGCGACT TCGATTCAA					100
40	TCAATGTCCC	CTGAATGCCA	CAGAACCACT		
AGCAGACGCT GCTCTCTCAG TCTTAATGGA GTGGCCCTCT					150
GGAAACAGCC GAGCTTGAA AGATGCATAT CAAATGAGTA CAGACACTTG TAGCATTAA					200

509

TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG 250
CCCCAGGTGA CCA 263

5 (2) INFORMATION FOR SEQ ID :1005:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1005:

CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG 50
CTTCCATCTC ACTATTCTT GATCATTATC TCTGAAGTCC CTACCTGCAC 100
20 TCCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCCAA 150
GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTCGAATT 200
25 GTAAAATCGT GAGCCACTCA TATTCAAAC TAAAAAAAGAA CAGAACTTTT 250
ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTTACGGAT CAATGTCRAA 300
CGCTTGCATT CATAAAG 317

30 (2) INFORMATION FOR SEQ ID :1006:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

510

	CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTCCCT GGAATGCCTT	50
	TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCACTCCTT AACAACCTAG	100
5	CTGAGGTCTT ACCTCATCAG GATTTGATCC CCCAAAAAGA TTTGTCCCTC	150
	TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA	200
	TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA	250
10	GAGTCTTGT CTAAATACTC AAAACCTGT TTACCAT	287

(2) INFORMATION FOR SEQ ID :1007:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1007:

25	GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA	50
	CTGTCTCATC GGGGCACCTG TAATAAGCAT CTTGATGCCA CTGAATGCAA	100
	TGCTGTATTG AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG	150
30	TAAAACTTGA AGCCCTTGA AGGACCTAAC CAAACAAACAC AAGGATGAAA	200
	ATAGATCAGT ACAACTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA	250
35	TATTCGGATT TTACCGTAAG GAA	273

(2) INFORMATION FOR SEQ ID :1008:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

511

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1008:

	TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA CCTATGGACT	50
	TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC	100
10	CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGACACACAGA GTTCATGTTT	150
	GCGCCCTCTC CCTGCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGCA	200
15	TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG	250
	GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG	300
	CAAAAAAA	308

20 (2) INFORMATION FOR SEQ ID :1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1009:

	GAACCGCCTC TGTTCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA	50
	GCAGTTTGA AAACCTGGATT AGGAACCACT AATGAAAAAG AACAGACTCA	100
35	GGGACAAGTG TTTGGCGGGA ATGTGTGAAG AGGTAACCAA TGAGTGTAC	150
	TGAATCACAC TATTACACAG ATGAAACAAA GCCTTTA	187

40 (2) INFORMATION FOR SEQ ID :1010:

512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1010:

10

AAGAAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG	50
ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA	100
AAAACAGCTC CATA GTCAAT ACCCATGAGT GATCTTAAAT ACGCACAATT	150
AAGCTACTTC TCCTTGATAT TACCT	175

15

(2) INFORMATION FOR SEQ ID :1011:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1011:

30

TGAAAAATAT TTGGAACCTCT TTAGTACAGA ACAGTTCAA TATGAGTTAA	50
GAATCATGCG ATGACTACCA AAAAGCTAAT CGGATCCCAG GCTGGGGTAA	100
CAGAACCCAGA GCAGCTCAGC TGGGGAACGT GATAGTGATA ACTACTTCGT	150
ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG	200
TATTTTAT	208

40

(2) INFORMATION FOR SEQ ID :1012:

513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1012:

10	ATGATATCTA GACTACCA GT ATT TTGAA TGAGGCTTTC TTAGGAGTAT	50
	GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCTCTG	100
15	ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG	150
	ATGAGGATGA GGGATTGAGG GATGCTATAA GCCA	184

(2) INFORMATION FOR SEQ ID :1013:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1013:

30	CTTTGACATT TGATCAGACC AAACAGTGCT GTTTCCCGGG GAGGAAACAC	50
	ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTAC CTCATGTTTC	100
35	ATACCTTGTT TATCAAATGA GCGACTAAA ATGATTTAAA ATAATGCTGT	150
	TCTTTAGTAG CAACTAAAAT GTGTCTTACC GTCATTTATA TCTTTGTCAC	200
	CGGAAAGAAG CATTGGAT ACTTTACTGC GAGTCAAAAA TCAATACGCA	250
40	GAATGGCATT TGA	263

514

(2) INFORMATION FOR SEQ ID :1014:

(i) SEQUENCE CHARACTERISTICS:

- 5
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1014:

	CAAATTAAGT GCCAGAACATGA TGCAGCCCCGC TCTCACCCAGG AAGAACGACA	50
15	TGTGAGAAAA CTTATAGCAG ATGCCAAAAT GTCAACCCAC CATGTTATTT	100
	AAAAAAAAAAAT ATGACCAGGA TACAAGGACA CTTCACCGTT TTTAACCCAC	150
	ACAAGGTCAG GTAATGTTA CCTTGAAACA CAATCGCATA TGACCCTTA	200
20	TGCCACTCAC CTAGGCCTTT AATAATGAG	229

(2) INFORMATION FOR SEQ ID :1015:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1015:

35	GAAAATAATG ATTCAATTAA CGGGGTATTT CTTATCCAGT CTTTCATTCT	50
	ATGTAAATTG TGTGTGTGTC TATATATGCG TGCATGTCTC TCTCTACATG	100
	TATATGTGCA TATGTATGTA TATATATGCA TATGCACATA CATGCCACAC	150
40	ATGCACATAT ACACACACTC ATAGAGAACAA AAATTATTCC GAATATTCA	200

515

TGAGGTTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA

246

(2) INFORMATION FOR SEQ ID :1016:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1016:

15	TTCATAATCG CTGGCACTGA ACAAAAGTTGC AGAATTCTTT GCCAGGTACT	50
	TTAGGAAATC GTGAAGATAA TTGAGTAATA AAGCAAGGCT CTTCTCATCC	100
	AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG	150
20	ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA	200
	GAATTTCAAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC	250
25	AACATTACGT TGAAGTATTTC TTTTATACTC GCCACAA	287

(2) INFORMATION FOR SEQ ID :1017:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1017:

	ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA	50
40	CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTGAA ATGCTGTTG	100

516

	TCAACATTTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG	150
	TTAACCAACAA TCAGTTCTAC ATAATTAAAC AGAAAACATC TGGTGGCACT	200
5	TTTAAATGTT TAAGGACAGC ATTTCACAAA CTAAGCCCGC CCCCAGTCCC	250
	ACTGCAGCAG GAGAAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA	299

(2) INFORMATION FOR SEQ ID :1018:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1018:

20	ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT	50
	GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT	100
25	TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAACAG	150
	TGGGTTTGAG GTGGGCCCAA GAATTCCCT TTTAACAAAG TTCCCAGAAG	200
	ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTC	250
30	AACAGGACAA TCTAAAGTGC TCCC	274

(2) INFORMATION FOR SEQ ID :1019:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

517

(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:

	TTTCTTGTC CTTGACAAAT ATTTATGGAA TGCCGAAAT TATGGAAAAA	50
5	CAATTCCAAT GTTACCGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC	100
	GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG	150
	CATCTTCTAC CACTTTAAA GGCTACCACG AGACGGGTG GAAATGCCAA	200
10	AAATGGCACC TCATCTTGAA TCAAAGATTG AG	232

(2) INFORMATION FOR SEQ ID :1020:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 133 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:

25	AACAGTCCAT GCTGATCTTA GTAACTATGA TGAAGATGGT GCTTGGCCTG	50
	TTCTTCTTGA TGAATTGTT GAGTGGCAA AAGTCGTCA GACATCATAG	100
	CAAGAACTAT GTGAAGAAAA TGCAAACCTT TAC	133

30

(2) INFORMATION FOR SEQ ID :1021:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 280 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:

518

	TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT	0
	ATTTAAAATC ACAAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG	100
5	ACTGTTGAAA GTTTAAGTAT TAGTAAACTT GAGTTACTTT TTCTTCAAA	150
	TTTCACTCCG CTTCCCTGCA TTTGAAGCT GCTCTTCTG GTCCTACCCA	200
	CCACCCCCACC AACAAAGACTT GTGTTGTTA ATAGAAATAA TTTATCAAGG	250
10	TATTGGGGAT CCATTGTCTA TATTTAAAAC	280

(2) INFORMATION FOR SEQ ID :1022:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1022:

25	AAAATAAAATA ACTTCTTAGA TTTTGACTG AAAAGATCTG AGAATGTTCT	50
	GCCAAACAGC CGACCAACTG GTGCAAAGG TTAAGGCTGA CTTGACTTAG	100
	CAACCTGCAG CACAACCAAA AACACTGATG CAGTCAGAG CTCTTCAAAT	150
30	GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTTA	200
	ATCCTCTAGA CAGTTTTCTT TTTGTTTGC ATGCATCCCG TTCCATTTTC	250
35	ATTACGGGCA TCTATTCCCTT GATCAATTAT GTGCTTGCT TTTTAATCGG	300
	TTTT	304

(2) INFORMATION FOR SEQ ID :1023:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs

519

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1023:

10	TTTCTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA	50
	CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC	100
	GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG	150
15	CATCTTCTAC CACTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA	200
	AAATGGCACC TCATCTCTGA TCAAAGATTC AGAGCAT	237

(2) INFORMATION FOR SEQ ID :1024:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 320 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1024:

30	GGCATGATTA TTAGAAACTA TTTAAGCTTT TTTCTTGAA AAACAAGCTC	50
	CTTTTACAGA ATATAAACAA CAGTAGTGCC TGTGGTTTAG CCCAGCAATC	100
35	TTGATGACTA AAAGTAGCTG ATGCATTGTG CATATGATGC TTGAGATGGT	150
	TTTGCAAAA GCAGAAATCG CTGCAAGGTA ATCACAATAG ATAAAAGTGG	200
	TATTTTAAAC CTTTGAAATA AATGGATGTA ACTGTACCTT GGTACAGCTT	250
40	TTCACTTGTT TAGTTTTAA ACGTTAGTAT AAGATTAGGT AATTGAGGGT	300

520

TAGAGCCAAC AGGAATCTGC

320

(2) INFORMATION FOR SEQ ID :1025:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1025:

15	TTCTGGCACC ACATTCAATA CTGATTCAACA GGGATCTAAA ACATTCTAGT	50
	TATTCAGTCA CTCTGTCTTG TGTGGCAGAT AGGACTTATG TATCTTCAGA	100
	ATATTTGAGG AGTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAAC TG	150
20	TTCCACAAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT	200
	CT	202

25 (2) INFORMATION FOR SEQ ID :1026:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1026:

	ATGGTAGAC AATATCATAA GAGTTTCTG ATAAAAGATG CTTTTAAC	50
	CTGACTCCCCA GTCACAATTT TGGCATCTCA TCCATGGGAA AAAAATAGGA	100
40	AACTTATACA TTTCATAAAC TAAAGGTCA CCACACACTG CCAAAACGT	150

521

TTTTATAAAT TGAGACCTAC TTACATCACA TCGGTTTCC AAAGAGAATA 200
 CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA 243

5 (2) INFORMATION FOR SEQ ID :1027:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1027:

TATTTGCATT GAGGAAATAT TAATTTCCA ATGCACAGTT GCCACATTAA 50
 GTCCTGACTG TAGGAAACAC TGATTTGTA AAGTTGCCTT TATTTGCCTGT 100
 20 TAACTGTTAA CTATGACAGA TATATTAAG CCTTATAAAC CAATCTTAAA 150
 CATAATAAAT CACACATTCA GTTTAAAAAA AAAAAA 185

25 (2) INFORMATION FOR SEQ ID :1028:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1028:

GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTG TGGAGCCACC 50
 TTACTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGAGCAG GAAATTTATG 100
 40 ACCAGAGTGG GGTCCCAGGC CACAGGGAGA TGTCTATCCA CAAGGGATGG 150

522

	TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG	200
	TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCT TCTCCTCAGC	250
5	CTTC CATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT	300
	CTGTTCACAG TT	312

(2) INFORMATION FOR SEQ ID :1029:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1029:

20

	ATTATTTATA AATTTTAGTG AGCACCAACCA AAGTTAGGAT TCAATTGAGT	50
	TTGAATTCAA ATTCAATTCAA AAGTTGCACA AATTTATTTC TTTTTTCCTG	100
25	AACATTCCCTT TACTTCAGAT TGACAATTCA TTCTATTTAG AGCGCTATTT	150
	TAAGAAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA AGTAGAATT	200
	TATACAGATG GAAAAAGA	218

30

(2) INFORMATION FOR SEQ ID :1030:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1030:

523

	TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGGTTAAC ATTGAATAAA	50
	ACTACAAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT	100
5	TTCTTAGTTC TTGGACACA TCCG	124

(2) INFORMATION FOR SEQ ID :1031:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1031:

	TTTGCCAAG TATATGTAGT GCAAATATTT TCTTCAGTC TGTAGCTTGC	50
20	CTTTTTATTT NTTAATGGGT ATCTTAAAAA AAATGGAAGT TTTAAGTTG	100
	AATGGAATTC AGTTGTTTT TAAAGCTTGT GCTTTTGTG TTCAACTAAG	150
25	GGATATTAGC TTACCATTTT TCTCGGTGA ATATTATGTG TTTATAGACA	200
	AGAAATGGTC ACTAAAGCAA AATAACTGAA AATTATC	237

(2) INFORMATION FOR SEQ ID :1032:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1032:

40	ACAGCAACCG GCACTCACTT GGAATCCCAG TGTTCCGAGT TCTAAGGCCA	50
----	--	----

524

CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA	100
GGCAGTTCCCT TGAAGACTGT TTTAACATA CCAAAGGAGG ACAAGCT	147

5 (2) INFORMATION FOR SEQ ID :1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double.
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1033:

AGGCCTGCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA	50
GAGGGGGGCA CTAGAACGAA TATCTCGAA ACTTCTTCGA CTGTCGAGAC	100
20 TTTTTACTCA TAATTGCGTT CAAGCCAAT ACGGAGGCGC ATTTACAAAA	150
CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA	200
25 TCCTCTGTCC CTACTCCCTC TCCTAGGACA CCGCATTA	238

(2) INFORMATION FOR SEQ ID :1034:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1034:

TCCATGNCTC NTGGTCTCTG TGCNCTTGNC AGGGGCATGC CAGGGCCCTT	50
40 GGACTGTGCA GGG	63

525

(2) INFORMATION FOR SEQ ID :1035:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1035:

CGACCGGCGC TCAATGGCGA AATTCCGAGC CAGAGCTATT GGTTGAATGA	50
GTAGCGCTGA TGGTTTAGAT AATAACTAGT ATGGGGATAA GGGTGAGCAG	100
GCGGCCCTTG AGGCAAGAAC CGGGTTAGAG CATCTCTACT TTAAAAGCCA	150
AAGCCTATAA CGGTAGCGTC TACATCACGA	180

20

(2) INFORMATION FOR SEQ ID :1036:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1036:

CCAAATACGA TGACATCAAG GAGTCGATCC GTCAGCGTGA CTTGAATACA	50
CCACCGCCGA CGACCCGAAA GCCTGATGAG GAGAAGTCCA GAATCAGGAA	100
CAACGGCGAC ACTCGACTAA CCATTTAAA CCAATTGGAA CC	142

40

(2) INFORMATION FOR SEQ ID :1037:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs

526

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1037:

10	CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCCGA GCCTGGAGGC	50
	TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG	95

(2) INFORMATION FOR SEQ ID :1038:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 195 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1038:

25	ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT	50
	TTGACAAAAA CATAACACACA TAGTACAGGT AGAACATATA ACTGGTTGAT	100
	GCTAAATAAC AGATCCAGAT AATTTCAAT TTGAATTAGC AGCAGGGAGT	150
30	CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTCAGT	195

(2) INFORMATION FOR SEQ ID :1039:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

527

(xi) SEQUENCE DESCRIPTION: SEQ ID :1039:

	GGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGGAACACAT	50
5	TACAGAATTTC ATCATCAAGC AGGAGGTTTT TTCCAGGTTTC TAAGATGAGG	100
	TTAAGTTTCT TAACAAAAGA ATAAACAAC GTGACTCTAT CTGTCGGGG	150
10	AGGGTCTAGA CAGAAAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAAA	200
	CGAGACTTTG ATGGAGAC	218

(2) INFORMATION FOR SEQ ID :1040:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 318 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1040:	
25	TTTATTATTT TGAATGATT TATGGTTTC TACACAATT ACATCACAAAC	50
	ATGTAATTT TAGCAGTAAC ATCTGATTCT AACAGGCACAT CATGCTATT	100
	CTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATT CCTTAGTTGG	150
30	CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTTAAAGATG	200
	CAAATGCCCTC TGAGTGAACT GTACTATCCC ATCACTGAAG CCCACAGGAA	250
35	CAAGTCCTAC AATTTAAAAA AGGCTCGATG GAAAAATTTC TCAATCCTGA	300
	AATCCCCCTAG GGAAGGGG	318

(2) INFORMATION FOR SEQ ID :1041:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 199 base pairs	

528

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1041:

	ACGTACCGAG CCGTCGTCGC GGTGCTTGAG CTTGAAGGCG AGATAGCCGA	50
10	TGCCGCCGAG GCGGTGGACC GCATCACGGT GGCGCTGACG AACGCCGAGAT	100
	TCAGCAGCAG CGATGCCATC AATAGCAGCC TGATCGGACG CATGACCGAC	150
15	TCTCCCTGTG AGCGGAGGTT GGGGGCCGA TCTCCGCCG GTGCCGGGC	199

(2) INFORMATION FOR SEQ ID :1042:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 300 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1042:

	GCCTCTAACAA AAACCTAGGCT GTCCCGGACC ATGGTAATAG AATTGTTTAC	50
30	CTTTATACCA AGAAGGTTGG GAAAGCACCA AAATCTGCAT GTGGTGTGTG	100
	CCCAGGCAGA CTTCGAGGGG TTCTGCTGT AAGACCTAAA GTTCTTATAG	150
35	ATTGTCCAAA ACAAAAGAAC ATGTCAGCAG GGCCTATGGT GGTTCCATGT	200
	GTGCTAAATG TGTTCGTGAC AGGATCAAGC GTGCTTCCT TATCGAGGAG	250
40	CAGAAAATTC GTTGTGAAAG TGTGAAGGC ACAAGGCACA ATGTCTGGAA	300

(2) INFORMATION FOR SEQ ID :1043:

529

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1043:

10

GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAACAGA 50
GTCTGGGATG AAGCGGCCTC CTCCCTGTCT TGCCCTCCAA AATTGAGTCT 100
15 GGCCTGATTC CTTTGAGGAG CAAATTTAC AATCATCCCT CACCCCTAAC 150
CACGGTGAAA CTGGAAAACC 170

15

(2) INFORMATION FOR SEQ ID :1044:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1044:

30

GGCCCCCCCCT GGGGACTGCT GGTTTCCAGG GGCCACCCCC CCTCATCCAA 50
AAGAAGAACATC AAGTTTTGTT TTCCCTGTGGT TCCCTTGCTC TCCCCGGCCT 100
35 CACCTCGAGC TTCCACTTGG GCCCTTCCCC ATGCTTCTAC TTGAGCCCCG 150
CCTGCCTCAC CGTCTGCCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT 200
GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCAT 250
40 TTTTTTTTTT 260

530

(2) INFORMATION FOR SEQ ID :1045:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1045:

AAATCTATAA	TTTTAAGGGC	TTAACCTGTG	ACTTTAATAA	GCTGGAACAG	50	
15	TCCACTGAAT	GGGTATAATG	AATTGCAGTA	TATACGTATG	ATCGCTTTT	100
	AAGTGATTAT	CTTTTCTTTC	GTAAAGTCAT	GTAAATTCAAT	AAATTTTTG	150
	20	GCAC TGATGT	GTTG			164

(2) INFORMATION FOR SEQ ID :1046:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1046:

TCCCTCCTT	CCGAAC TGGG	GCCCCATCCT	CTCCAGAGTA	TCCAGGGCTT	50	
35	CTTC ACTCCC	GGGTACCTGC	CCTTCGGCCC	CTTTTCACCA	CAGCTGTGCT	100
	ACTGTCAACC	AGTCTTGCT	GCATAGGCAT			130

(2) INFORMATION FOR SEQ ID :1047:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

531

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1047:

	GCTTAACCTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC	50
10	AGTGGAAAGCA AAATTCTCAC AATGAATAGC AGTCTTTCCA GCTTCTTGA	100
	CACGGATTTT CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG	150
15	TGAATCTCCA TTCGAGGAAG GGGAAAGAAGA GCTCGGAGGG TGACAGCCTC	200
	CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCCTT CTTCCCTCCTG	250
	ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA	285

20

(2) INFORMATION FOR SEQ ID :1048:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1048:

	TAAAACGTGAC CTAGAACGTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA	50
35	CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC	100
	CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC	150
	GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC	200
40	CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA	233

532

(2) INFORMATION FOR SEQ ID :1049:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1049:

	ACTTTAATTT ATTCGGATG CCGGAATTGT GCCCAGAGTT TCTCCTGAGC	50
15	TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCCTCTG	100
	AACTCTGAGC TGTCCCTTCC TGACAGGCAC TTTCCATAGC ATCTGCCCTGC	150
	TTAATTCCCTC ACGACTCAGA AATGTTAACG GCACTGTCGA GTGCTGTGAT	200
20	CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTTC	250
	GAGATAGAGC TAGAGAAGAA AAGCAGCAA ATTGGTCA TAC	293

25

(2) INFORMATION FOR SEQ ID :1050:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1050:

	AAAACATAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA	50
	GCACAAATCT ATTATTAGTG AATGAAGTAT ATTCTGGCA GATAAATACC	100
40	AGATCAAAAG TCCTGTTCA GTAATTGAT TAAACTGTAG AATACTAAAA	150

533

AATAAGTTAT TTCTACAGAA ATCTTGAGG GGAGCAAAAA ATCAAATCAC 200
AGTATATAACC TAATGGCTA 219

5 (2) INFORMATION FOR SEQ ID :1051:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1051:

AGCGACCGGC GCTCAAGTGG AATTCCGTGC AGTGTGAT TTTTCGTTT 50
TGCAGATAGTT TACTGAGAAC 70

20 (2) INFORMATION FOR SEQ ID :1052:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1052:

ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTTCAAGA ATGGTACCTC 50
35 CTGCCGATGA TTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC 100
CTTCCAGAGA AGATAGGATG TGAGTGAGTA AGTTATGTAT AATAATTAA 150
TCTCAAAATA ACCACGTCCT TGATACCATT CCCTGTATAC CAAGGAAGGG 200
40 TATT 204

534

(2) INFORMATION FOR SEQ ID :1053:

(i) SEQUENCE CHARACTERISTICS:

- 5
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1053:

	ACTAAACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT	50
15	AAGAGAGGGC ATGGAACAGA TTAAAGAGAAT TAACACGGAG AGGAGAGCAG	100
	AGGTATAAAA GGTATCCAAG AAAAGTAAAAA CATAACAAAGG CAATTCAAAT	150
	CAAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC	200
20	CATAACCGAC AGAAAGTACC GGAATACCAAC CGACACTGAT GTCTTCCAAA	250
	CG	252

25 (2) INFORMATION FOR SEQ ID :1054:

(i) SEQUENCE CHARACTERISTICS:

- 30
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1054:

	AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA	50
	CATCTGCTTA TTAAACACTG AAGTAAAAGA ACTAATCCAG TTTGCAGTCT	100
40	TTAGAGGTGT TTAGTATTTC ACTCCGTTCT GATGGAAGCA CTTTGAATGC	150

535

TTGCATGGAG ACATAAAACT GAATATTTAA TTGACAATAG ATCATGCGCC 200
TGTATTTATA AA 212

5 (2) INFORMATION FOR SEQ ID :1055:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double.
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1055:

ATAAAACGTGTG CTAAC TAAAG TTTTTATTTC ATCAATATAA AAGCTGTAAA 50
AAAAC TGAGG AGAAACCACT TGCCAAAAAG ATGAAAGAAA AACAACATAG 100
20 AAAACCTTTA AACACGGCAA AAGTCAGTTC ATAATAAGT AACTCATCTC 150
AC 152

25 (2) INFORMATION FOR SEQ ID :1056:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1056:

AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGTT 50
GAAACCTGAC AACTGACTGT TAGCCTTGTC ATCATCCTCA TTGGAGATGG 100
40 AGATGTTGTA GTCGGAGCCT CATTCCCTCC GGGGCACTGT TTCTTCTAAT 150

536

GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG	200
GCAAA	205

5 (2) INFORMATION FOR SEQ ID :1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1057:

GAGAGAAGAG CGCTTTTCTG GGCTCTTGGT TACTCCGTCA GAGACTTTGC	50
CCTTTGTCTG TTTAAATACA CTGGGAGCCA GAGCTGATTG CCCACCTGCT	100
20 GCTGTGGTTT TCCGCTTAAC ACAGGAGAGA TGAGTTGGTC TGGTATATTT	150
GATAGCAGGT TTTAAAATGA ATCC	174

25 (2) INFORMATION FOR SEQ ID :1058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1058:

TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAA	50
GCTTTAAAT ACCATGTTGA CAGCATTTG AATTGTTCA TAGACGTACT	100
40 TATTTAACTG ATGCGAACAT TCACA	125

537

(2) INFORMATION FOR SEQ ID :1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1059:

TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTCA AATACTGTCT	50
15 TAGTATATTA AACTCTTTG AAATAGATAA CAAAAGCACC ATGGGACTCC	100
GTTGAAAAC TAGGTTTGTG CCTTCTAAAA TTTCTAAGTC CTTCAATTATG	150
ACTATAAAGA AAAAAGGTTC ATCAATTCAA AAAAAAAATCC TGATTCTTCA	200
20 AAATA	205

(2) INFORMATION FOR SEQ ID :1060:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1060:

35 ATCTCACAGA TTCTTTTCA CAGATTCAAT CATGTTGAGT GAAAGAAGCC	50
AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTG	100
40 AAAACTAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG	150
GTGAGTGTCA TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTTATAAT	200

538

ACTTGGATT TGGGTCTAC	GCTGGCAGG GGAAGGCATA CATTGCAA	249
---------------------	-------------------------------	-----

(2) INFORMATION FOR SEQ ID :1061:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1061:

15 TAGCACATTG CATCCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA	50
AAATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCATAT	100
GCAGAACATCAG TGGTTGAAAA AGGAGAAAAGA GAGATTTCT TTACAAAAGC	150
20 TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC	200

(2) INFORMATION FOR SEQ ID :1062:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1062:

35 GCGCACAGCT GAGAACATCCTT GGTCTTGCT CACTTTGGAC TGGGACAGTG	50
GATGCCCATC TAAAAGTTAA GTGTCATTTC TTTTTAGATG TTTTACCTTT	100
ACAGCCATAG CTTGATTGCT CAGAGAAAATA TGCAGAAGGC AGGATCAAAG	150
40 ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTCCT	200

539

(2) INFORMATION FOR SEQ ID :1063:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1063:

	TATCAAATCA TGAGTTGAAA GATTTGACT ATTGAAAACC AAATTCTAGA	50
15	ACTTACTATC AGTATTCTTA TTTTCAAAGG AAATAATTTT CTAAATATTT	100
	GATTTTCAGA ATCAGTTTT TAATAGTAAA GTTAACATAC CATATAGATT	150
	TTTTTTTACT TTTATATTCT ACTCTGAAGT TATTTTATGC TTTTCTTATC	200
20	AAATTCAAAT CTCAAAATCA CAGCTCTGAA TCTTAGAGTA TCATAA	246

(2) INFORMATION FOR SEQ ID :1064:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1064:

35	CCCTCATGTG CCAGTCGGT CTGCCTGCAG AGGCTGTGGA GGCGCCAAC	50
	AAGGGCGAGT GGGAAAGCGTT TGCAAAGCCA TCCAGAACAA CGCGCAAGTT	100
	TGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA GAGGAGGACA	150
40	TGGAGCCTGG ACTGAGCCAC	170

540

(2) INFORMATION FOR SEQ ID :1065:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1065:

CTCTCCCCCA CAGGTTCTCA GCAGTTACTA AGATGTCCCC TGATTCATT	50
15 GACCTCTGTG TGTCTTCAGT CCTTGACCCCT TTAAGGCTCC CTGGTGCCAG	100
AATGTCTGCA GCTGTAGGAT CAAAGACCCCT TGGGGGAAAAA ATCCATTCTC	150
AAAAGAGAGG AAGATGGGGT G	171

20

(2) INFORMATION FOR SEQ ID :1066:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1066:

GAGTCTATAT CCCTTACTCA GTGCAGTTCT CAAAGTCCTT TGTATGTCGT	50
35 ACAGGATCAC ATCTGTACAT ATCACACTCT TGTGGGGTAA GCCCAGAAC	100
TCATACACAG CTTCATGGGT TTACTTTCCC AAGCACTTCC TCCCTCCCTG	150
CAATATCTCC CCAGCACTTT CTGCTTCCTA TCAGCTTCC CCTTTTCAA	200

40

C

201

541

(2) INFORMATION FOR SEQ ID :1067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1067:

ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT	50
GAAC TGAAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG	100
GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTCTAA CGCGCGCGCG	150
C	151

20

(2) INFORMATION FOR SEQ ID :1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1068:

ACTGTGTCA T GTCAGGTTAG ATCTGAATCT CTAGGAGAA AGCTTTTTG	50
ATCTGTTGC TCCTTGAGT CTCCCTTTA CTTTACAAT AGAAAACCAA	100
TCGCATACTT CACTTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC	150
TACCGTTGAA ATTTAGCATA ATATTTCTCC CTTACCTTTA CGTCCTTTA	200
AAAAAAATAGG ACTATAGTAA GTCCCTCCGTG TCGGTGGCAT GTTTTTGGAA	250

542

ACTGACTTTA AAGAAAACAT ACA

273

(2) INFORMATION FOR SEQ ID :1069:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1069:

15	CAATCTTGCT TATAAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCA	50
	TCCTGGTGCA ATTGTGATT TTTTTAGCC AAAATGAATG GCAAACCTCA	100
	TTTAGAGCAA AGTAAGTATT AGAAAACCCT AGGAACCTT AATCAACGTT	150
20	TATTACACTT TTATAAAGGC AAACTACCGC AAAGAGCCC	189

20

(2) INFORMATION FOR SEQ ID :1070:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1070:

35	TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT	50
	TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG	100
	TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC	150
40	ATGAATCACG ACTTCTCATC CCGTTTATC AGAGTGCATA TACGTCCCTAC	200

40

543

TTAAGGAAAA GTAAAACAGT CATTACGAA AGAAAGTCAA TCTGTATCCT 250
AAGCATTATA ATAAAAAGTC AGAAGGAATT 280

5 (2) INFORMATION FOR SEQ ID :1071:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1071:

AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC 50
TACCGCCAGA AGCTAGAAGC AAGCACTTCC TCCTAACCGA GTTTTTGAAA 100
20 GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCCTCTA CGGGGGAAAA 150
GATGCCAGT AACAAACCAT CTAGGGAGAC AGCCTTCTAA CAG 193

25 (2) INFORMATION FOR SEQ ID :1072:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1072:

AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCCAGATA GGCCACGCGC 50
AGCTCCAGCA TCTTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC 100
40 CACTCTGCAG CCATAGGCC CACTCTGGCC CCGGGTCACT CCCTCCAGGG 150

544

TCAAGTTCCC CTCGAGATTC ACATC

175

(2) INFORMATION FOR SEQ ID :1073:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1073:

15	AGTGCCCTAC TCTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG	50
	GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG	100
	GTGGACAGGC TAATTTTCC TTGAAAATGT GGCTTCTTCA ACTCCTTCA	150
20	AATTTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT	200
	TCTCTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA	250
25	TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA	300
	TCTATATAGC ACATAGTGT TAAAGACTAA TGAATGCAA	339

(2) INFORMATION FOR SEQ ID :1074:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1074:

40

ATTAATTATG CGGTCCCTCCT CCTGGCAGCT GGACACCACT TTGAATCTTC

50

545

	CTTGAGCTC CGGAAAGTTG GTAATTACAA CTTGATATTT CTACATGGAA	100
	ATCAAGAAC TCGGACCCAA CTTGGTCAA AGACGGATCT CCGCCGATTC	150
5	TGACGGCTCT CCAGGTTTG TC	172

(2) INFORMATION FOR SEQ ID :1075:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1075:

	AGAGTAGGAA GAGGGAGGGG AACAGGCATC TAAGATAGAC TTTCTCCATC	50
20	TGTTGGGAGC CTGGGCAACT AGGAAAGAAG CCTTTTCAT ACACTTCAGT	100
	CGTATGACTG AGCTGCTTGG CAGGGCACTG GAAACGACGA ACTCGCGCAG	150
25	CCTGCAAATG AGACCACCTCT CATTTCAG TTTCGATTTG ATTCACTCAC	200
	TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG	250
	GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTACACGTTG CTACTGATG	299

30

(2) INFORMATION FOR SEQ ID :1076:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 283 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

546

	GCCCTCATCG GCGATACTGG AGGTTCGCTT TCTCAACCCT GTGGGCTTCA	50
	CCCCAGACAC GCCCTGAATC GTTCATGTT CCAGCATGCC TGAGACAATC	100
5	ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GCCAGATCTG	150
	AATGCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG	200
	CGAGGTAGTG CTCATGCCTG GCGAGACGTG TTGTGCTTAA TGAAGCCCTA	250
10	TCATTGAAAG TATTGCTATG AGCAGTGCAG AAA	283

(2) INFORMATION FOR SEQ ID :1077:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1077:

25	ACCAATCAAG TACACTAAAT TAGAATATTT TAAAGTATG TAACATTCCC	50
	AGTTTCAGCC ACAATTTAGC CAAGAATAAG ATAAAAACTC GAATAAGAAG	100
	TAAGTAGCAT AAATCAGTAT TAAACCTAAA ATGACATATT AGAAACAGAA	150
30	GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA	200
	GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTCAGGC TGGAAAACATA	250
35	TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAAATG AAAGCAC	297

(2) INFORMATION FOR SEQ ID :1078:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

547

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1078:

	AATCTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC	50
10	AGTGATTGAA CCTTTATTAT TTACCAAGCTA ATATAGTAGG CCCATAAATA	100
	GGTTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG	150
	TAGCGCTACT ACCCATAACCT GCTAGCAGTC AAGGTTCAGA TAATCATAAC	200
15	ACGCCAACCA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA	250
	GTTTATATCT AAAGCCCAGT TTCTTTGCT TAATATTAGA G	291

20 (2) INFORMATION FOR SEQ ID :1079:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1079:

30	AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAAC ATAAGCGGGG	50
	CTCACTCACCC CACCACATTA ACACCAACGAA ACGGGTAATC TAACACGAGA	100
35	AAACACCCCTA ACGTTCATAC ACCCCATACCA CCATTA	136

(2) INFORMATION FOR SEQ ID :1080:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

548

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1080:

	CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT	50
10	GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA	100
	GCTGCGGTAT TAAAAAAATC AAGAATGGAA GCGTTCCCTCA ATTGTGGTTG	150
15	AGAACATACAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT	200
	CGCGCGTTTT TCATGGTTCG CATCTGCCGT GTATGCAATG ATTCTCAACA	250
	CACATTGGAG TCACGCGGCC TGCCTAAGAG TATGAAGGTC TTCCGTAAA	300

(2) INFORMATION FOR SEQ ID :1081:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1081:

30.	GTAAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAAA GTTTTACTAA	50
	AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT	100
35	ATTGGATGAG ATTTGTTTG CTCCTTACTT TCTTTGTATA CAGCCAAGCC	150
	TGAAAATCTC TAGACATTG CTGAAATTGA TGAGAGCATG CACAGGACGA	200
	CTGAAGGTGC TGGACATGA	219

40 (2) INFORMATION FOR SEQ ID :1082:

549

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1082:

10	ATTTGGGAA AGTGAGCATG AAGAACGGAC TCAGAGCTGC CAGGTACCCG	50
	AGTCTCAGGC TCTGACATCT CTTGGGCC CCTTCTGCCA CAACTTCTTG	100
15	CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGGCCT	150
	GCAGCACAGG CGTGTATCCT CTCCAAAAAG CTGCTGCTCA TTTCTGGCCC	200
	CATCTGCTGC TATCTTGCC AGTCAGCCAT CACAGTTGG CATCATCAGA	250
20	GTCTCAGCTA GAGGGAGCGT GTCATTTCTG CCTTAGTGGT TTGCCTGCGA	300
	CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACCT	350
25	GTCGGAAAGTT	360

(2) INFORMATION FOR SEQ ID :1083:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1083:

40	CATACATATG AGACTGAGCG GATCAAAGTT TTACTACAAG TCTTTATGAT	50
	CTTCAATTA AATACACTCC AAGACATCGA GTTGGCAGA TATTGCGCCC	100

550

5 GCCGTTTGC TCTTCTTATC TTTGTATCCA GCCAAGCCTG AAAAGTCTCT 150

AGACATTTGC TTGAAATTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT 200

5 GCCGGACATG ATTCTCTGCT TTCTGGTTCA ACAAAAAAAA AAAGTTCCAG 250

(2) INFORMATION FOR SEQ ID :1084:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1084:

20 TNCTAGATAAC NTCCCTCTGT CTCACATTCA TAGTGTGTTG TTGTCTAGTG 50

TATGAAGTCT CACNCAAGGA AACTGTNCAG GCAGAGTTG GGGAGAGTGA 100

AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNNTCCA NCCATTATTG 150

25 GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAAGA NTTTTTTAAA 200

AAATTAAAAA GAGGATTTT AAAAGGAATA TCTTGTCAA AATTNTTAA 250

GTTTTAATAG G 261

30

(2) INFORMATION FOR SEQ ID :1085:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

551

	GCAATCCATA AGTGTCCCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT	50
	CTTCATGATC TTTTCGATT TTAAAATGTC ATGCAATTT AGAGAAAAGC	100
5	TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA	150
	TCACTTTTC ACTTTCCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC	200
	TTAATACACC AGACAAGAAC ACACATGAA TGCGAGACAG AGGGAGACAG	250
10	AGGCAGAAATA	260

(2) INFORMATION FOR SEQ ID :1086:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 213 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1086:

25	AAGACGTGGA TTTGCTGGAA GACACGGATT TCCTGGAAAGA CCTGGATTT	50
	TCGGAAGCTA TGGATTTGAG GGAAGACAAG GATTTCTGG AAGACATGGA	100
	TAATCTGGAA GACATGACTT TGTCGGAAAGA CGTGGACTTG CCGGAAGACA	150
30	CGAATTCCT GGAAGACCCG GATTTTCGG AAGCTATAGA TTTAAGGGAA	200
	GACAAGACGG ACT	213

35 (2) INFORMATION FOR SEQ ID :1087:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 256 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

552

(xi) SEQUENCE DESCRIPTION: SEQ ID :1087:

	TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG	50
5	TTTAGGCATT TGGAAAATCT GGTCACATC ATAAAGAACT TGATTTGAAA	100
	TGTTTTCTAT AGAAACAAGT GCTAAGTGT A CCATATTATA CTCGACGTCG	150
10	ATCATTCTC AGTCCTATTT CTCAGTTCTA TTATTTGAGA ACCTAGTCAG	200
	TTCTTTAAGA TTATAACTGG TCCTACATCA AAATAATAGA AATTACGTTT	250
	TTTTTT	256
15		

(2) INFORMATION FOR SEQ ID :1088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- 20 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1088:

	TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC	50
30	TTAACGCACA TCCCCAAACG CGGGTCTGG CCCCAGACAG GGAGACCAGG	100
	GCTCTGACAG TGACAGGTTTC TTCCCTCTGA AAAAAGAATA GAAGAGGGAGC	150
	TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA	200
35	AACACAGAAG AGAGTGTGTC TTCCCCAACC TCTACCAGAC AGTAGAGAAA	250
	CTGAGGCCAG AGGC	264

40 (2) INFORMATION FOR SEQ ID :1089:

(i) SEQUENCE CHARACTERISTICS:

553

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1089:

10	GACCTGGAAT TTGTTTCGT CTGTTCAAGTA GACTCCGATT TCAGAAATATG	50
	TCGGAATTTC AGACTCCCGA ACTTTTGAGA ATGTCATTAC AGGAACCTTG	100
	TTTACATACC GAGCTGTTAG CCCCAGTCAC TGGGTCCGAA ATTACGCCGA	150
15	TACCGAC	157

(2) INFORMATION FOR SEQ ID :1090:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 366 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
25	

(xi) SEQUENCE DESCRIPTION: SEQ ID :1090:

30	GCATATAACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGAA	50
	CGAGGAAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT	100
	AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAAACG CGATGAGAGA	150
35	GAAACTTGAA AAGTCAGAAA ATAAGTCAT ACCGCAATTA ACCTTTGGT	200
	CAAGTAATGG AAACCTTTGA CTACTAGTGT AAGTCAAAAG ACAAAGGACT	250
40	CCAGCAAGAT GAGAGATTTC TCTATTTGT AACGAGTAGT CCACCGATCG	300
	TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAA	350

554

AAAAAACATA GATGTT

366

(2) INFORMATION FOR SEQ ID :1091:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1091:

15	GGTCTGAATC ATGAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC	50
	AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCCATTTC GCTCTTGTCA	100
	CACCATATGA AGACATCAA AAACACTTAA GGATTCGAGA AAGAGAACAT	150
20	CTTTTGTAA AGAAGAGAAT AAGATTTGG AAGAAAAAGT AATAGCAAAT	200
	TTGAAGAAGA AACAAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCATA	250
25	TCATGCATAT CGAGAGGTTT ACATTGATAG AGATAATTG AAGAGCAAAT	300
	GGACA	305

30

(2) INFORMATION FOR SEQ ID :1092:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1092:

40

AAATGGAAGT TGAAGTGAGT GTGGTTCCA GTACAGGGCA TCTGGCCACC

50

555

	TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT	100
	GCCAGAGACA GCCAAACACA GGAGACATGA CAAATTACTA TCATCTTTG	150
5	CTTCTTTATT TTTATTATTA TTATTTTCT TTTTGTGGAG AACAGCGTCT	200
	TGCTGTATTG CCCAGCCTGA TCTCAAACTC CTGGGCG	237

(2) INFORMATION FOR SEQ ID :1093:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1093:

20	AGAAATTTAT TGCCTCACAG TTCTGGAGCC TGGAAAGTGC ATATCAAGGT	50
	GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA	100
25	GGTCTCTGTC CTTGGCTTGT AGAAACACGC ATTCTCTGG TGGATCCACA	150
	CAGTCTTCTC CATGTGTATC CTTCCCTCAG TTTCCCTTAT AGGACACCAAG	200
	TGATGTCAGA TTAGGGATCG AACCCAACAA CCTCATTGAGTTACTCAC	250
30	CTGTTGAAA ACCCTATGTC CAAATACAGT TATAGTGAA GGAACTAGGA	300
	CTTAGGGCTT ACAAAATATGG AGTGGGGCAT CATCCAGACC ATACCAATTAA	350
35	AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CATAACACACA TTAAGGTTG	400
	TGGGATTCAAG AAAGGTATAC	420

(2) INFORMATION FOR SEQ ID :1094:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs

556

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1094:

	GTTCCTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA	50
10	CAGCAGGTAC CCAGTAGAAG GAAAGGTGGC TGATCATTTT TCCATAGGAG	100
	GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC	150
15	AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT	192

(2) INFORMATION FOR SEQ ID :1095:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 228 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1095:

	AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT	50
30	ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCCTCCTCCC	100
	ATTGTCCACC CCCATCCTCC TTACCCACGAA ACACATTTTT CACCAGCATT	150
35	GCCAAACAC TTGGGATTCC TGCGCATGGC TTTGCTTAGT TTGCTCTCT	200
	GCTTCTTGGA TACCTCCTTC AGGAAATC	228

40

(2) INFORMATION FOR SEQ ID :1096:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 198 base pairs

557

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1096:

	ATTTTTATG GAAAAAGGGG GATAATGCAA AATAGCAAA ATTGTAAACA	50
10	AAGTAAAGA TTATCTTCAT CTAAACCTTA AGCTGACAAT TTAAAACACC	100
	TTGTGCATAA TGCAGAAAAA AACTGTCCGT TTGACTTCAC TTTCATTAC	150
15	ACTGCTCCCT ACGCATGAGA AAGACCAAGAT GTCTGGTTTC AGAGTATT	198

(2) INFORMATION FOR SEQ ID :1097:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 118 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1097:

	TAGAGAGAAG TTGATATATG AAGATAGGGT GGACAGGACT GTGAAGGAGG	50
30	CTGAAGAAAA ACTGACTGAA GTGTCACAGT TTTTTCTAC AAAACTGTGA	100
	CACTTCAGTC AGTTTTTC	118

35 (2) INFORMATION FOR SEQ ID :1098:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 138 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

558

(xi) SEQUENCE DESCRIPTION: SEQ ID :1098:

5 AAAACTGACT AAAGTCANTG TGTAATACGA AAACCGAACCA CTCCAGCAGT 50
CCTATTTTAT NTNTTCCAAC CTAGNNCACCC CAGGTGACGC NNNGGACTCG 100
TCNCAGGTGT TTNGNACTTG CCGCCCCACN GGCNAAGG 138

10 (2) INFORMATION FOR SEQ ID :1099:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1099:

ACTCCACCAC TGGGNCCGCC ATGTTTGGG TNNGNGCAAT GCGCTGTCTG 50
TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT AACTGACTG 100
25 ACACTGGGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG 150
G 151

30 (2) INFORMATION FOR SEQ ID :1100:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1100:

TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT 50

559

	CGTGTAAAGTA CACTCTATAT TGGCACACA TAAAATTAAC TAGTGACGCA	100
	TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT	150
5	CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG	200
	C	201

(2) INFORMATION FOR SEQ ID :1101:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1101:

20	TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT	50
	CGTGTAAAGTA CACTCTATAT TAGCACAAACG ATAAAATTAA CTAGTGATGC	100
25	ATTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG	150
	TATCACTGGA GGACTGGGN CAGGACCTGA CCTGGTGGTA CCAAAATCCA	200
	TGAGGCNGNA AT	212

- 30 (2) INFORMATION FOR SEQ ID :1102:
- (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

560

	CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG	50
	GTTCGTGTAA GCACACTCTA TACNNGCACA ACATAAAATN AACTAGTGAT	100
5	GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC	150
	AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN	200
	GAGTGGAAAT TCCANCAT	218
10	(2) INFORMATION FOR SEQ ID :1103:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1103:

	GTAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT	50
25	TCGTGTAAGT ACACTCTATA TTAGCACAAAC GATAAAATTA ACTAGTGATG	100
	CATTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA	150
	GTATCACTGG AGGACTGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC	200
30	ATGAGCG	207

(2) INFORMATION FOR SEQ ID :1104:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

561

(xi) SEQUENCE DESCRIPTION: SEQ ID :1104:

	GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG	50
5	ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC	100
	TCTGCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCCCTGAAC	150
10	AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT	200
	CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN	250
	GTGNAGGCC	259

15 (2) INFORMATION FOR SEQ ID :1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1105:

	ACATGACCCC TTGGACTGAA GGCCTCAGT AGTAAAGGAG TGTCTATGCAG	50
	GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA	100
30	CGGGGACTTC TGGGAGGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG	150
	CAGGGCAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC	200
35	ATTTGTTTCG NGTTGAAAGA CCCAGAAAAT	230

(2) INFORMATION FOR SEQ ID :1106:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

562

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1106:

	ACATGNCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT	50
	CAACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA	100
10	GGACTTTTGG GGGGAGTGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG	150
	GTNAGAGGGG GCT	163

15 (2) INFORMATION FOR SEQ ID :1107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - 20 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1107:

	ACNTGATGAT TGCCATTATT GTGTGCTAGT GGCTAGAGGT AGACCCAATA	50
	GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCATTCTC CAAGCCCCCT	100
30	GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA	150
	GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT	182

35 (2) INFORMATION FOR SEQ ID :1108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - 40 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

563

(xi) SEQUENCE DESCRIPTION: SEQ ID :1108:

	CCCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTCAACAC	50
5	ATGTCGCACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT	100
	TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCCAG	150
10	AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTTGTTT	200
	CGNGCCTTGA AAGA	214

(2) INFORMATION FOR SEQ ID :1109:

- | | |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 133 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 20 | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :1109:

25	ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTCAACACAC	50
	GTCAACACAC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC	100
30	ACAGGACTTT TGGGGGGGGT GGACAGGTAT TAT	133

(2) INFORMATION FOR SEQ ID :1110:

- | | |
|----|-------------------------------|
| 35 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 156 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

564

GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTCA	50
CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA	100
5 TGCACGGGG ACTTCTGGGA GGAGAGTGCA TAGGATACTT GTCTGTGACT	150
GGAATG	156

(2) INFORMATION FOR SEQ ID :1111:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1111:

20

GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCGC	50
AGGTGCCTCA AAGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC	100
25 ATNAAGGATG TTATAGATAT ATCCAAAAGA AAATAAATCA TTCTTCAAAA	150
AGACACATAC ACTAACACGT TCATGGAGCA CTATTCACAC AGCAAAGACT	200
CGATCAACTC ACACACTCAT GAATGCGGAT CGAAATAGAA GATGTGGTAT	250
30 GCATACACCA CGAAATACTA CGAGCCATAA AA	282

(2) INFORMATION FOR SEQ ID :1112:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 181 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

565

(xi) SEQUENCE DESCRIPTION: SEQ ID :1112:

	TAATTAGTTT AACCACTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA	50
5	ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT	100
	CAAAAGGAAA TAAANNGNCN TGTNAAGAC CATAACNAT NGTCCATCGG	150
10	AGCCCGTATN CACGCAGCTT GTCATAACTA T	181

(2) INFORMATION FOR SEQ ID :1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1113:

	ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG	50
25	AACTAAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA	100
	TAGATATATC CAAAAGAAAA TAAATCATTC TTCAAAAAGA CACATACACT	150
	AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA	200
30	CACTCATGAA TGC GGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA	250
	AATACTACGA GCCATAAAAG GCGAAATC	278

(2) INFORMATION FOR SEQ ID :1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- 40 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

566

(xi) SEQUENCE DESCRIPTION: SEQ ID :1114:

ACCTGCAAAC TTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG 50
5 TGAGCCATAC AGTTTTGTT GCAACTAGTC AACTCTAAC TNACGTGGAC 100
AGCATGTAAA GAACGAGAGT GACTG 125

10 (2) INFORMATION FOR SEQ ID :1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1115:

GTAGCGACCG GCGCTCATGG AATTCCGGGA CCTGCAAAC TTTTGAAAG 50
ACCAGATAGT AAGTATTTA TGCTTGTGA GCCATACAGT TTTTGTCAA 100
25 CTAGTCAAAC TCTAACTCAC CGTGGACAGC ATGTAATGG ATGGGAGTGG 150
CTGCCGG 157

30 (2) INFORMATION FOR SEQ ID :1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1116:

CCTGCAAAC TTTTCTGTA AGACCAGATA GTAAAGTATT TATGCTTTG 50

567

GAGCCATACA GTTTTGTTG CAACTAGTCA ACTCTCAACT NACGTGGACA 100
GCATGTAAAG AACGAGAGTG ACT 123

5 (2) INFORMATION FOR SEQ ID :1117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1117:

ACCTGCAAAC TTTTTTGTA AAGACCAGAT AGTAAGTATT TTATGCTTG 50
TGAGCCATAC AGTTTTGTC CAACTAGTCA ACTCTCAACT CACCGTGGAC 100
20 AGCATGTAAA TGGATGGGAG TGGCT 125

(2) INFORMATION FOR SEQ ID :1118:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1118:

35 ACCTGCAAAC TTTTCTGTA AAGGACCAGA TAGTAAGTAT TTTATGCTT 50
GTGAGCCATA CAGTTTCGT TGCAACTAGT CAACTCTCAA CTTCACCGTG 100
GACAGCATGT AAATGGATGG GAGTC 125
40

(2) INFORMATION FOR SEQ ID :1119:

568

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1119:

10

ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT	50
CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT	100
CAAAGAGCCA ATGAGAAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA	148

15

(2) INFORMATION FOR SEQ ID :1120:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1120:

30

AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT	50
AATCAAGAAA AAATAGCACC AACAAACAATG AGGAGAAAAT GGAAAAAGGG	100
CAGAGTATTT CAAAGATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT	150
TAAGCCTTCA GTTTGCCCTG TAAGCAAACG GAAGACGTGC AAGTCATCCT	200
TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAACT	240

35

40

(2) INFORMATION FOR SEQ ID :1121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs

569

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1121:

	AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG	50
10	GTGAGACTAA TAAGAAAAAA TACACCAACA ACAATCCGAG AAAATGGAAA	100
	AAGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG	150
15	ATTTTTAACG CTTCACGTCT GCCCTGTAAG CAAACTGAAG ACGTGCAAGT	200
	CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGCA ATGAGAAGGG	250
20	ACAG	254

(2) INFORMATION FOR SEQ ID :1122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1122:

	AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC	50
35	NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAAACAT GAGGAGAAAA	100
	TGGAAAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA	150
	ACGAATGATT CTTAAGCCTT CACGTTGCC CTGTAACCAA ACTGAAGACG	200
40	TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAC	250

570

GAG

253

(2) INFORMATION FOR SEQ ID :1123:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1123:

15	AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AATGAATCCT	50
	GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAAATCCGA GAAAATGGAA	100
	AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT	150
20	GATTTTAAG CCTTCACGTC TGCCCTGTAA GCAAACGTGAA GACGTGCAAG	200
	TCATCCTTTG	210

25 (2) INFORMATION FOR SEQ ID :1124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1124:

	AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC	50
	CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA	100
40	TGGAAAAAAGG GCAGAGTATT TAAATGATTA CGGAGACGGG CAAACCAATC	150

571

AACGAATGAT TCTTAAGCCT TCATGTTGC CCTGTAAGCA AACTGAAGAC 200
GTGCAAGTCA TCCTTGAGAC CCTGGGAGAG T 231

5

(2) INFORMATION FOR SEQ ID :1125:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1125:

AAGTCCCATC AGCAACCCGT TTTTACCAAG ATGTCACTCA AGAATGCC 50
20 CGTGGCCCTC CAGTTCCCTGC GCACTAAGAG CGTCCCGCT 89

(2) INFORMATION FOR SEQ ID :1126:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1126:

AAGAAAACCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA 50
35 ACCAAAAACTT CACGACCCT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC 100
ACCAATACTG ACAATTGTAG CGGTAATACA TACAATGATT TAATAAGCCT 150
40 ATGCTACTGG ACACATGCC ACACAAATAAT ANTCAANRTGT NTYGTAGGC 200
CTACT 205

572

(2) INFORMATION FOR SEQ ID :1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1127:

	GCAAGGCCTG GCCGACAACA CCCTTATTGC TAAAGTAAAT AATGNCGCGC	50
15	GGGCCCTGGA CCACCCCTCTG GAAGAAGATT GTACCTTGGA GCTTCTCAAG	100
	TCTGAGGATG AGGAAGCTCA GGCAGTGTAT TGGCGCTTTA GTATCACATA	150
20	A	151

(2) INFORMATION FOR SEQ ID :1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1128:

	GAGCACCCCCA GCCCATAACA CAGAACTCGT CCCCTACCC CCCTCAGCAA	50
35	GCCGGAGAGG CTAGCCCAAG TAATCATTAAY AACAGCCGCC CGAGAGCAGC	100
	CCCAGTAGCA GCCCCATGGC CGGGCGGAAC ACCTACATCG ACAACCTCAT	150
	GACAGACGAG ACCTGCCAGG ACCGAGCCAT TGGGGCTGC AAGGCCTCRC	200
40	CCTTCGTCTG GGCCGCCGTC CCCGGAGAAA CGCTCGT	237

573

(2) INFORMATION FOR SEQ ID :1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1129:

GCCTCGTGGAA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG	50
CACCAACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT	100
CCTTAAGATC ATCCAACATAT AGGATG	126

20

(2) INFORMATION FOR SEQ ID :1130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1130:

GCCATCTTCT GTAACAAAAT AAATAGTGTC AAGCACTAAA TATATGCATG	50
AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT	100
CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG	150
TTTATTTGCA AGGATTTTC TTTCGRGGGC GGAGGGGAGA GAAAAAGTAAA	200
TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCCTT YGTATC	246

40

(2) INFORMATION FOR SEQ ID :1131:

574

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1131:

10

CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTAA	50
TCCTCTGTCT GACCATGATT TTTTCCCTCA AATACAACCA CTCCTCGACT	100
TTTCACCCTC AAAGTATAAA AAGTATGAAA NATAAACAAAG CTCTTGACT	150
GTACACTTAG AAGTGTACAA TTAAAGCATT ATAGAGCTAT CTACACACCG	200
ATAAAATCCC A TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG	250
TGCAGACAGA ACTAAAACCA ACT	273

20

(2) INFORMATION FOR SEQ ID :1132:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1132:

35

GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG	50
TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAATCCTAT TCAGTGCTCC	100
CTTAGACATT CTTCCAGGCA GGATCAAACCT CAAAGGAAAA GGAATTGTG	150
AAGCAAACCA TGGCTTGTC ACAGTAAAGT AATTGTCACT CTCAACCCAG	200

40

575

AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA	250
AGCCAATGTA TCTGACCCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT	300
5 ATTTCTGTTT GTTAAAAAGT TCAGAATTT	329

(2) INFORMATION FOR SEQ ID :1133:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1133:

CCCCGAGCTA GTTGTCCCGA CCTG	24
20	

(2) INFORMATION FOR SEQ ID :1134:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1134:

GAGGATCCAC AAACCATGGA ACACCTCTCGC GGCTGCCACT CCCCCATGAC	50
35 CACCCCTACAG GCCCTAACCC CAGCCCCTCA CGTTATCGTC CAGCCACAAA	100
TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG	150
40 CGGGCCCTGC CGGGCACCCC AGCTTCTCG CAGGCACCAA AAGCGCAGTT	200
CCAGGAATCT CTACCCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA	250

576

CCAAACCTCG CCAGAAGGCT TCTTTCGGG TTGATGCCA TCTATTY 297

(2) INFORMATION FOR SEQ ID :1135:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1135:

15	GCCGCTTAC TGCTCAGTTC GGAGCTACCG CTTCGAAAGC AACAAAAAAG	50
	CNTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA	93

(2) INFORMATION FOR SEQ ID :1136:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1136:

30	CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG	50
	TTGTGGAGA TAACGGTGGC ATAGTTCCCT GATGCCCGGG CCAGCTTGCC	100
35	ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA	150
	TGGTCCCCAC AGGGAGCRCA TTGCCAATGT TGAGCTGGGC CTTCTTGCCG	200
	CAATACACAA ACTGGCCCGT GNGAATGCCC TCGGGGGCAA TGAACAGTTC	250
40	CGCCCGCTTC TTAAACCAAG ACAGATCCCG GAAGGCCGCC TGGGCAAGGG	300

577

GCCCTCRAA CCCGGGCTA TACACGTCAA AATC

334

(2) INFORMATION FOR SEQ ID :1137:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 199 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1137:

15	CGAGGATCCG CATAACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG	50
	ATGAAGAAC TCCAAACCTT TTGACAGCTC CTCGGGTNA AACCTGGNAY	100
	AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT	150
20	CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT	199

(2) INFORMATION FOR SEQ ID :1138:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1138:

35	CGAGGATCCA AATACCATGG CGCTCCCTCC TCCCGAGCGC CGCTCCCGT	50
	GGCACCCGGC TCGCTCCGAG TTTCAGGCTC GTGCTAAGCT AGCGCCGTCG	100
	TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC	150
40	ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG	200

578

	TTGTGCCTGG AGGTGAAGGG GAAGATGATC AGTAGGACAG AAGGTAACAT	250
	TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG	300
5	AAGG	304

(2) INFORMATION FOR SEQ ID :1139:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1139:

20	GAGGATCCGG GTACCATGAG AAACTTGAA GCCAGAGATT TTAAACAATC	50
	AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAAACAAA	100
	CAGCTGTACC AACGAGTAAC AAAGAACAG TAAATCTTCA TCTTAACAAC	150
25	CTTTAATAGT TATCTAAATG CAGAGTTGT TTATGAAATG AACCAAAGCA	200
	GTTTGTCACT TCTTACTATA AAATACCGAA AATAAAGTGC AAAACTTAGC	250
	CACTACTGGC TAAAGAAACT AAGTAAA	277

30

(2) INFORMATION FOR SEQ ID :1140:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1140:

579

CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCAA	50
AAGAGAGCTC CCTGAGAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT	100
5 TTTAGCAGAG CAAATTTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGG	150
GTACCCAAAC CCTCCAATTG CCAACGCGGT CTCAAGTTCA GACTGGGCTC	200
CAGCTTCT	208

10

(2) INFORMATION FOR SEQ ID :1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1141:

CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG	50
25 CCAGCTTATA ACTGTCATCT TTATTCAATAT GGTCTCCAAA TCCCACGATG	100
TCAACAATGG TTAACATTGAG CCGTACATTG CTTTCCTGAA GCTCATAACT	150
TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACHTT	200
30 TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT	250
GTCTCACCAA TACAAAGGAT GTTG	274

35

(2) INFORMATION FOR SEQ ID :1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- 40 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

580

(xi) SEQUENCE DESCRIPTION: SEQ ID :1142:

	GCCTGCACAT TGACTGTGGG AAACCTCGGAA ACAAGCTCAC ATCTCCCCGT	50
5	GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAAC TG CAGTTGCCAC	100
	CTTCCTCTAT GCGGAGGTCT TTGTTGTGTT GCTTCTCTGC ATTCCCTTCA	150
10	TTTCTCCTAA AAGATGGCAG AAGATTTAA AGTCCEGGCT GATGGAGTTG	200
	TTAGTGTCCCT ATGGTAACAC CTTCTT	226

(2) INFORMATION FOR SEQ ID :1143:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 168 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1143:

25	RGGRTCCRNG TGCCRGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRC	50
	TGRCRCGNTG NCNGTGAGGR CRTGNRGNC CRTGCGAGTG GGCTTACCGN	100
30	TAGGTTCGGG AATGACCTTG CYMACGNENN YGACAGCTAA GTRGRNGCRG	150
	GNANGRTGNN GTGGAGRG	168

(2) INFORMATION FOR SEQ ID :1144:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 256 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

581

(xi) SEQUENCE DESCRIPTION: SEQ ID :1144:

	CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT	50
5	TCTTGAGGGGA CCTTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTGC	100
	CAGGATTGAA GGAAATCGAC TGCCTTCACT CTTCCCTGAA ACTTTGAAGT	150
10	CCACATAAGG GCTTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT	200
	AAACAACCTT ATAGTGTGTT CGCTTTGAAT TGTATGAATT CTTAGAACTG	250
	AGAAGT	256

15 (2) INFORMATION FOR SEQ ID :1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1145:

	AAACACAAGG CTAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA	50
	GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG	100
30	TACCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT	150
	GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG	184

35 (2) INFORMATION FOR SEQ ID :1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

582

(xi) SEQUENCE DESCRIPTION: SEQ ID :1146:

	CGAGGATCCG GGTACCATGG CCCAAAGAGT GAATGATGTA TCCCAGGGCG	50
5	CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG	100
	ATTTCCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT	150
10	TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG	200
	GTGCTGAGAA GAATGCACAA G	221

(2) INFORMATION FOR SEQ ID :1147:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 255 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1147:

25	CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT	50
	TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT	100
30	TAAGGGATTCT CACATTCAAGG ACAGAGAACCA AATTTTTTAA TGAATCCATC	150
	CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC	200
	RRTMATTCTT AACANCAAAC NGMGMCTGNN NTCCCRNCTT ATAACCMAAA	250
35	GATNT	255

(2) INFORMATION FOR SEQ ID :1148:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 230 base pairs
	(B) TYPE: nucleic acid

583

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1148:

	CGAGGGATCCA GGTACCATGG ACGATTACA GCCCCTGGCC ACTGGCCATT	50
10	TCCAGTGGTA GGGAGCACAC TGRTCACATT CGAGACCCAC CACGTTGAGC	100
	AGACAAAGGC AGCCTCCACT CTCCCTCGTCA CTCAACATGT ACCTCCGTCC	150
	CCCAGGATGT TGTAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG	200
15	AGTCGGTGAC GCCCGATTTG GATCGGGTGT	230

(2) INFORMATION FOR SEQ ID :1149:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 223 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1149:

30	GTGCCGTTGG TCCTGTGCGG TCACTTAACC AAGATGCCTG AGGAAACCCA	50
	GACCCAAGAC CAACCAATGG AGGAGGAGGA GGTTGAGACG TTCTCCTTTC	100
	AGGCAGAAAT CGCCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG	150
35	AACAAAGAGA TCTTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT	200
	GGACAAAATT CGATATAAAA GCT	223

40 (2) INFORMATION FOR SEQ ID :1150:

(i) SEQUENCE CHARACTERISTICS:

584

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1150:

10	CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAACACTC	50
	GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGA ...TC CTAATGCCCT	100
	ATGATCACGT GGAACTAACA T CAATGACA TGAAGAACGT GCCAGAACCC	150
15	TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT	200
	CTTTATGTCC AAGAACAGG ATGCCATGGG TATTCGTGA NGCTATTGAA	250
20	NMTRAGGRMA GNCTGNAAGG TM	272

(2) INFORMATION FOR SEQ ID :1151:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 25 | (A) LENGTH: 140 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1151:

35	TGAGGATTAA TAGATTANAG CTAGAGTTCA CATTATGG ATTACAACCA	50
	AAAAAAACCT GAAAAGAAA AAAAACAAAA AAGCTCAAAA GCAATCACAA	100
	GGATAGTTGA ATCCCTCTT AAACCCCCAA AGCAACCCCC	140

40 (2) INFORMATION FOR SEQ ID :1152:

(i) SEQUENCE CHARACTERISTICS:

585

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1152:

10	AAGGATCCGG GTACCATGTA TTCCCCGGT ATCAGCAGAG GCGTGTACGG	50
	GCACTGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGGAGG	100
	GTCACCAAGG TAGATTCCA GCAGCCTAGT CCAGCTGAAC GCTTTCCAGC	150
15	CTTGCTTTT AGCAGCTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC	200
	TTTCATTG	208

20 (2) INFORMATION FOR SEQ ID :1153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1153:	
	CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCCTGGA	50
	TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG	100
35	CTACTGAACT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACCTCCAG	150
	GCCCCAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCGGCCAG	200
40	GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCA	250
	GAMCCCNMAC AGGGCTRGGG ACTG	274

586

(2) INFORMATION FOR SEQ ID :1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1154:

	GAGGATCCAC CGACCATGGA ACAC TCTCAA TGGCTGCAAC CACCCCGTGG	50
15	CCCCCCTACC AGCCCCAATC TCCAAACCCC GCACGTCGAT CATGACGCCA	100
	CCAACAGCTG CAGCCCCTGA GATCTTCACC TTAGACCCCTC TCCCGAAGCC	150
	CGCAGCCGCC CCTGCGAACCC CTCCAACCTCG TTCACACCGGG CCGAAAGCCT	200
20	ATTCCCAGGA CTCTCTGCCCTACGTGACC GNCCCTAGCT GCTAGTCGAG	250
	AATCCGAACT CCGCTCC	267

25 (2) INFORMATION FOR SEQ ID :1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1155:

	CTCAAACCCC GNTTCCCCCC TAATAAGAGC AACTAAAAAA CTTCTGATAA	50
	CCACAATAAA AGCGTGCATT TGACCACAAT TCAAAAGCCA ACCCCTTCGA	100
40	AGGNGTTCT GATGAAAAG GACTTATGTT GAACGAAGCA GGAGTTAACG	150

587

CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC 200
CGTCTANCAA GGCAACGGCC GCCTTTGAAT T 231

5 (2) INFORMATION FOR SEQ ID :1156:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1156:

GCGCGAGCAC AGAGCCTCGC CTTTGCCGAT CCGCCGCCA TCCACACCTG 50
CCGCCAGCTC ACCGTGTATG ATGATATCAC CNCGCTCGCC ACCAACRACG 100
20 GCTCYAACMT GTGCAAGGCC GCCTTCAA 128

(2) INFORMATION FOR SEQ ID :1157:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1157:

35 GCCGCAACAC AACCCAGGGA GACTCAAGNC CACAGGGGCC CCCCCGGCTCT 50
GAGGGATTCA CCGTCGCCTC CCGGTCCCCG AAGGCCACCA AGGGCAGAAA 100
GGTGAGCCTT ATGCACTGCC TAAAGA 126

40

(2) INFORMATION FOR SEQ ID :1158:

588

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1158:

10

AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA	50
CCCCAAACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAAA AACCCCTCCT	100
15 T	101

(2) INFORMATION FOR SEQ ID :1159:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1159:

30

GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG	50
GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC	100
35 CCCACACACCG GTGGCGGTGC GGGTGAAC TG GAAGGGGAGG TCGAAGGTGC	150
CATCTTCTTC AGGCCCCCTCC AC	172

(2) INFORMATION FOR SEQ ID :1160:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

589

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1160:

	GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA	50
10	TGGTTATTTC CCAGGACCAC ACGATTGCC TACGTCACTG GAAGGCTATG	100
	TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG	150
	CTTTGACCCCT GTGATGCCAT TTTAATCAAC CCTGCTTGGT TTTAGAGGAT	200
15	TGCTCCCGTG GGTCACTTGA GGCAGGCTCC ACCTT	235

(2) INFORMATION FOR SEQ ID :1161:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1161:

30	GAGGATCCAC CAACCATAAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG	50
	TTAGATACAA ATGCAAAACG CTTCCCTAAAA AACGGCCTGA AAAAAAAACTC	100
	ACAGACAATG CCAAACCTTA TAGGCTCTGTA TTTTCCTTTA TACAAAATGC	150
35	CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAAGTCC ACATCTCTGG	200
	ATTACCTATA ACCGGTATTAA TGGGGTGTGT TTATACTGCC TAGAATGTTA	250
	ACCCCTCATAA AGCCTTAAAA GTACATTTGT GAAA	284

40

(2) INFORMATION FOR SEQ ID :1162:

590

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1162:

10

GCTCACATAA ATTTCTTCAC CGACCCTTTT CCTTCCAGCT TCCTTACTAT	50
AAAAAAACCCC ACA AATA TGTTCATCAT CATCCATACT AACCAACCCC	100
GTCACCACATCT CAATCAGCAG CAAGTCCTAC TCTCTGTGGG TGAAACCTTG	150
TTACCACCTC TAGGGGCAGA CCCCTTTCA GATATATTCA AGAGTTTAAT	200
ATCCTCCCAC TATAGCGCTT CGACTTTGTA TCTTCCTCTA TGGCTACCAA	250
ATTCTGTCCG TTGATAAGTA CTGGCTCTAA ACCATGC	287

20

(2) INFORMATION FOR SEQ ID :1163:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1163:

35

GAGGATCCAA AAACCATAAA ATTCAATCATC CCCAGCAGGT GCNCTAGCTA	50
TACTTTATTA CAGCAAARCA CAACCACACG CTGAMCTANN TCGTATAGAT	100
AAACACCAAT CATGGGTCCG CC	122

40

(2) INFORMATION FOR SEQ ID :1164:

591

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1164:

10

GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG	50
GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCCTCTC CACTTGCAAC	100
CTCCAAGACC ATCTTCTCGG CCATCTCCTG CTTCTGAAGC CT	142

15

(2) INFORMATION FOR SEQ ID :1165:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1165:

30

TATTCCCCCG GTATCAGCAG AGGCAGTGTAC GGGCACTGCT TTAAAACCTGG	50
GAAGGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC	100
CAGCAGCCCT AGTCCAGCTG AACACTTTCC AGCCTTGCTT TTCAGCAGCT	150
TTGAGGAAAA GTATACTGAT CCGTATGTGA AATTTCATC GCACGTAGCG	200
GATGAGAATA GAGAACTCA	219

35

40

(2) INFORMATION FOR SEQ ID :1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs

592

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1166:

	GAGGATCCAC CAACCATAAGA AAGGAAACAA CACTTGGAGT GAACCCGACC	50
10	CAAGCCACTA CACCCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAA	100
	AACAACCGGA AAATAGACCC GGACGAAGAT CAAAGNTNT CAATCCAAAC	150
15	ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC	200
	AA	202

(2) INFORMATION FOR SEQ ID :1167:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 159 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1167:	
30	GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAATG ACCTTTACGA	50
	AGACACGTCT GATAACCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG	100
35	GGACAGAATG AGAGAGGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC	150
	ATCTGGAGA	159

40	(2) INFORMATION FOR SEQ ID :1168:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 211 base pairs	

593

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1168:

10	CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG	50
15	CGATTGCCAC CGCTTCTCTC TAGTCTCACG AGGGGTTTCC CGCCTCGCAC	100
20	CCCCACCTCT GGACTTGCCT TTCCCTCTCT TCTCCGCGTG TGGAGGGAGC	150
25	CAGCGCTTAG GTCGGAGCGA GCCTGGGCC ACCGCCGTGA AGACATCGCG	200
30	GGGACCGATT C	211

(2) INFORMATION FOR SEQ ID :1169:

20
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1169:

30	GGATTTCCGG TCCTGGCTTT CTGATATTC TAAAATCGAC CTGGAATCAA	50
35	CCATTGACAT GTCCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC	100
40	CATGATGATG AGCTGGAAGG GCGCCGGATT GCCTTCATCC TGTACCTGGT	150
45	TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG	200
50	ATGAACACTT T	211

(2) INFORMATION FOR SEQ ID :1170:

594

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1170:

10

GAGGATCCGC GCAACCATAG AACTCACAAAC CCAGCCATAT ACCTCAGACA	50
CAATGGAATG GGCGGAGGTC GAGGTNGACA AACCCCTGAGT AATGTTGGC	100
ACTTCCGCAC CGGAGCTGTT CTTACCTTG ATAAAGTGGA TGTTATTGCT	150
ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC	200
CTATCCACCA ACGNCGAACAA ATATGCTGTT GCCAMGATTG AGCACGAGCC	250
GTGGGGCTC AACGGC	266

20

(2) INFORMATION FOR SEQ ID :1171:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1171:

35

GGCACAAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG	50
CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG	100
GAGAACATAT CCCACATTAG GAATTGATT AAGCCTGAGA GTTTGAGGGC	150
TTAACCTT TAAAAC	167

40

595

(2) INFORMATION FOR SEQ ID :1172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1172:

AATAAACCTC CCTATCACAG TGACCTACTA CCCGCGTGTG CTTATATAAC	50
TAATCCAGGA CAACCCACAA AAATTATAGC AACACACAAA CACACCGCTG	100
ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT	150
TACTGAGGAT ACGCAACTCA TAAAACCTCA CTTAAAGCAA CAGGGCAGAC	200
GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC	232

20

(2) INFORMATION FOR SEQ ID :1173:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1173:

GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT	50
CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC	93

40

(2) INFORMATION FOR SEQ ID :1174:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs

596

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1174:

10	GCCTTTTTT ACCCGCCGGA AGCTACAGCT TTTGCCCCCC CAAAAAAACC	50
	CCACCCCTTTT ACCCACCGCG GACCCAAAAA CAGCAAAAC CAAGGACCTC	100
	TCCCAACCCC AACCCCTCCT TTTTGGCCCT TCCTTCCCCC CCTCCCAGCC	150
15	CACCCCCAGA CACCTCAATC CCCCAAAAGG ATGCCCTAAA CCTCTCCTAA	200

(2) INFORMATION FOR SEQ ID :1175:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 121 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1175:

30	GAGGATCAA AAACCATGGC ATTCACTACG CCCAGCAGGT GTCCCAGCCA	50
	TGACTTACCA TAGCAAAACA CAACCACACA CTAACCTGCA TCGCCTAGCT	100
	TACTGATGAT GATGTCTGG T	121

35 (2) INFORMATION FOR SEQ ID :1176:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 26 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:

AACCAGACAC GCCGACCCGC TGAATC

26

5

(2) INFORMATION FOR SEQ ID :1177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1177:

GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG

50

20

TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT

100

CTCATAGCAA ACCTCGAAC TGAGGATGAG ATGGTTACAG ATAAAGCCTT

150

TCAGGATGGA TTMAAGNAMG CAGAGAGG

178

25

(2) INFORMATION FOR SEQ ID :1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- 30 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1178:

GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA

50

40

AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCCACAG TTTGCCGTG

100

TGTTATGCAT CAGTTATACA GGTATCCCAC CAAGTTCAAG TCAA

144

598

(2) INFORMATION FOR SEQ ID :1179:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1179:

	GACCAGGGAG GAGGTTAAC CAACTGGAC CCCCTCCGGC CTAGCCGCCG	50
15	AGGAGGTGCA TTGGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG	100
	TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCACCGCT TTGATTACT	150
	GATCTCGCTG AAAAGACAGA CGCTTTAGA TACCGAGTCG ATAGGGGTC	200
20	TGCGGTACTT TTCAGTAGAT AGGTGGTGCT TGT	233

(2) INFORMATION FOR SEQ ID :1180:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1180:

	CGAGGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC	50
35	CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA	100
	TAGCCCCAAGG GGAAGGTATT GTCTGGAACC AGAAGCCGCC GAGCCCCCTT	150
40	CTTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG	200

599

AGGTAGACGG GACCAAGATC TGCTG

225

(2) INFORMATION FOR SEQ ID :1181:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1181:

15	TGAGGGATTAA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATT	50
	GATGAATAAG CTTGATGTGG CCTAGTTTN NGNNNNNTGG NYATGGTNNA	100
	TCNNNTTANT TTTTGTTG TTGTGNATAT TATNGAATAR AMGAATRGNG	150
20	TTTAGAGTTT GGAAGCGGCN RNGCGTARMG NNACTCYACG CTCGCNNCTN	200
	TTGNNNNACA GMRGGNCTC TNNGRTGAGT GGRTNCMGTG GGMGGNNTCN	250
25	NNNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTTGNNGCTN GCT	293

(2) INFORMATION FOR SEQ ID :1182:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1182:

40	GAGGATCCGG GTACCATGGC TCTCTCTTTC TTTTTTTCT TTTTCTTGGC	50
	GGATGTGAGA GCTGCCTGAG ATTCAAGGTC ATCCGGCAGC TCAGTCCCCA	100

600

CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTTGCTGTTT TTCTTCTCA 150

GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCAATTCC 200

5 TTCTGGCTGT TGAGACCCCCG TGGACTCCCC TGGATTCCAG AGNNNTNATTT 250

NG 252

(2) INFORMATION FOR SEQ ID :1183:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1183:

20

ACGAGGATCT GAATACTCTG GCCTGCAAGT AGAGGCTAAT TCGATGTGTG 50

AAACTGTAGA TTCGGCTTAA GGTAATAAGTC ATTTATAGAC TATTCAATAG 100

25

AGTCAGACTG GTCGAGGCTG GTAAAGTGTAG CGGAACGGTT GCTGACTGAT 150

ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT 200

GT 202

30

(2) INFORMATION FOR SEQ ID :1184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

601

CAGATCCTCA GCTTCGTGG TTCACAATTTC TTTCAGTCTC TTA

43

(2) INFORMATION FOR SEQ ID :1185:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1185:

15 ACCGTCCTTC TGGTTCATCC TAGCAAAAT CTCACCATCT TCTATCAC

48

(2) INFORMATION FOR SEQ ID :1186:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1186:

30 ACATCATCCG AGTCCCCTCT ACAGTGTTCA TTGTGATCGT TGCATCCCCC

50

30 TGGTTTGGAA ATAAAATATA AACTGCCCGG CAAGAGATAA AATTGTATTT

100

TTTA

104

35 (2) INFORMATION FOR SEQ ID :1187:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

602

(xi) SEQUENCE DESCRIPTION: SEQ ID :1187:

CTGGTTCTGT TTCTCGCAGG TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG	50
5 AGAATCCTAT TCAGTGCTCC CTTAGA	76

(2) INFORMATION FOR SEQ ID :1188:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1188:

20 AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA	42
---	----

(2) INFORMATION FOR SEQ ID :1189:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1189:

35 GGCGGACGTG CGCGCCTTGT CTTCGCGCA CCTGGGCCTG AGGTGCGTGC	50
CTCCCCGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC	100
GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC	150
40 GCCAAGGCCT TTTATTTATG GCTAGTTGC TCTCGTGAAA TACTAACATC	200
GTTTTAATGG CACTCATCAA GTACGCAAAT GATATGATT AACCTGGCGC	250

603

AAT

253

(2) INFORMATION FOR SEQ ID :1190:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1190:

15	GAGGATCCAC CAACCATAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG	50
	TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAA	100
20	CAACTACTCC AATTGCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT	150
	GAATTTAGGT TGGTTACCAA TATCGGCATA AAATAAACTR TGTAAGGCTC	200
	AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT	250
25	TT	252

(2) INFORMATION FOR SEQ ID :1191:

(i) SEQUENCE CHARACTERISTICS:

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1191:

GAGGATCCAA CAACCATAGA GCACATAAAA ACCGCCAAC GATCTAACTA 50
40 ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC 100

604

TGCCGANAGC AAGTACATGG GGAGGATTAC TACTTCCTGG TTGCCAACCA	150
CCCTTCCGGC TGCCCTTG TGACTTG	178

5 (2) INFORMATION FOR SEQ ID :1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1192:

GGATCGGCGG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT	50
CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT	100
20 GCAACACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNNG	150
NGGGCA	156

25 (2) INFORMATION FOR SEQ ID :1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1193:

ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTGT AATACAGACA	50
TAAC TGCAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA	99

605

(2) INFORMATION FOR SEQ ID NO: 1194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:

NNNNTCCTTC TCCTGCGACAGACA

24

15

(2) INFORMATION FOR SEQ ID NO: 1195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:

TGTCTGTCGC AGGAGAAAGGA

20

30

(2) INFORMATION FOR SEQ ID NO: 1196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:

40

AANNTCTCGG ACAGTGCTCC GAGAAC

26

606

(2) INFORMATION FOR SEQ ID NO: 1197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:

TTNNNTCTCGG ACAGTGCTCC GAGAAC

26

15

(2) INFORMATION FOR SEQ ID NO: 1198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:

GTTCTCGGAG CACTGTCCGA GA

22

30

(2) INFORMATION FOR SEQ ID NO: 1199

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

GTTCTCGGAG CACTGTCCGA GAG

23

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:

607

(2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:

GTTCTCGGAG CACTGTCCGA GAC

23

15

(2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:

CTGCTCTGTCG CAGGAGAAGG AA

22

30

(2) INFORMATION FOR SEQ ID NO: 1202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:

40

CTGCTCTGTCG CAGGAGAAGG AG

22

608

(2) INFORMATION FOR SEQ ID NO: 1203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:

AGCTCGGCTC GAGTCTG

17

15

(2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:

GCGACAGACA GCAGACTCGA GCCG

24

30

(2) INFORMATION FOR SEQ ID NO: 1205

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

GATCCGGCTC GAGT

14

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:

609

(2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:

CCGAGAACAC TCGAGCCC

18

15 (2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:

GTAAACGAC GGCCAGT

17

30

(2) INFORMATION FOR SEQ ID NO: 1208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1208:

40

CGAGGTCGAC GGTATCG

17

610

(2) INFORMATION FOR SEQ ID NO: 1209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:

CGAGGTCGAC GGTATCG

17

15

(2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:

TACGTTCGAC AAGCTTGAAT TCGCGGCCGC TTTTTTTTTT TTTTTTTTTT

50

TTTTTT

56

30

(2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:

611

GCCWSCGCCG A

11

(2) INFORMATION FOR SEQ ID NO: 1212

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:

15 GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO: 1213

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:

30 TTGACACCAAG ACCAACTGGT AATG

24

35

In the above SEQUENCE LISTINGS, some sequences are preferred because they fall into the category of sequences referred to hereinbefore which exhibit no more than 90% homology to a human sequence known per se. The preferred sequences in these terms are all of sequences SEQ ID Nos 1 to 1193, EXCEPT FOR SEQ ID Nos:

40 85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595, 597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97, 89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

612

**870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291,
615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127,
1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.**

5

10

15

CLAIMS:

1. A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-
 - 5 (a) a sequence selected from SEQ ID Nos 1 to 1193;
 - (b) an allelic variation of a sequence as defined in (a); or
 - 10 (c) a sequence complementary to (a) or (b).
2. A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.
- 15 3. A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.
4. A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of 20 the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.
5. A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.
- 25 6. A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.
7. A nucleic acid sequence as claimed in claim 2 or claim 3 and 30 encoding at least a portion of a biologically active polypeptide.
8. A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.
- 35 9. A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.
- 40 10. A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

protein and said fragment or sequence.

11. The use of a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a
5 gene.

12. A DNA fragment comprising a gene obtainable by the use defined in
claim 11.

10 13. An expression vector comprising a fragment as defined in any one
of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2,
3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a
DNA fragment as claimed in claim 12, positioned such that that nucleic
acid sequence which encodes the polypeptide corresponding to said
15 fragment, sequence or DNA fragment is in operable reading frame with a
control or regulatory sequence.

14. A vector as claimed in claim 13, wherein said vector control or
regulatory sequence comprises a regulatable promoter.
20

15. Host cells which incorporate as a heterologous part of their
expressible genetic information a fragment as defined in any one of
claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or
7, or a DNA fragment as defined in claim 12.

25 16. A process for the production of a polypeptide comprising
cultivating host cells as defined in claim 15.

17. An antibody directed against a polypeptide obtainable by the
performance of a process as defined in claim 16.

30 18. An antibody as claimed in claim 17 and which is monoclonal.

19. A novel gene product or portion thereof encoded by a fragment as
defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as
35 defined in any one of claims 2, 3 or 7, or encoded by the gene
comprised in a DNA fragment as defined in claim 12.

THIS PAGE BLANK (USPTO)

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- BLACK BORDERS**
- IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- FADED TEXT OR DRAWING**
- BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- SKEWED/SLANTED IMAGES**
- COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- GRAY SCALE DOCUMENTS**
- LINES OR MARKS ON ORIGINAL DOCUMENT**
- REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)